

Access DB# 80372

CRFE

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: M. A. WALICKA Examiner #: 78201 Date: 11/16/02
Art Unit: 1652 Phone Number 305-7270 Serial Number: 09/724571
Mail Box and Bldg/Room Location: 10D06 Results Format Preferred (circle): PAPER DISK E-MAIL
10D10

If more than one search is submitted, please prioritize searches in order of need. ME

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Beta - seescase enzyme composition etc
Inventors (please provide full names): ANDERSON J.P. et al

Earliest Priority Filing Date: 06/15/1999

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 83
97.

Thank you in advance.

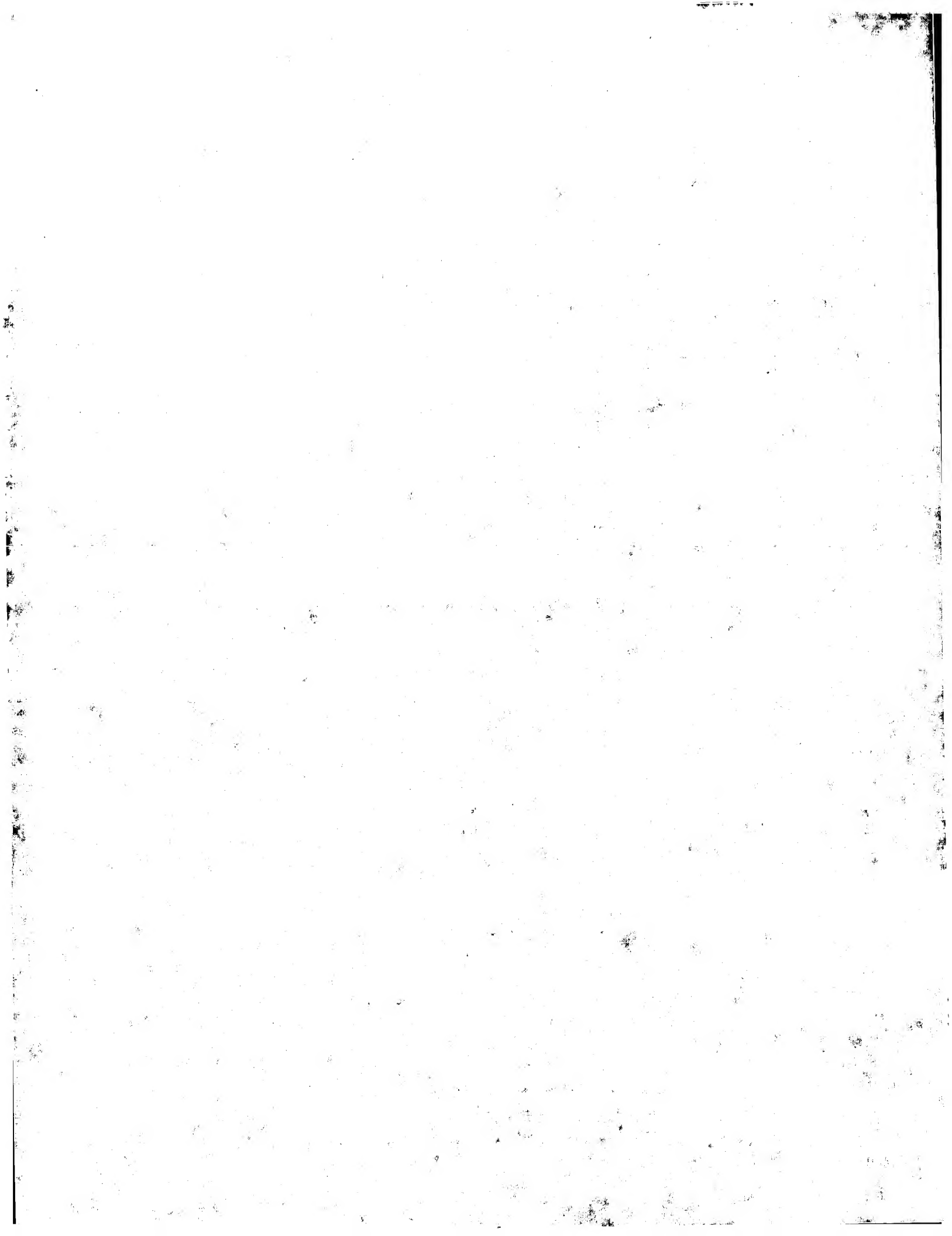
Malick

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AA 83-9 App No is 08/021, 954
AA 97-1 *CRFE*
08/445, 648

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	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>1</u>	Dialog _____
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Date Completed: <u>11/18</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>12</u>	Fulltext _____	Sequence Systems <u>CS</u>
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Online Time: <u>12</u>	Other _____	Other (specify) _____



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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:50:43 ; Search time 16.4348 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-09-724-571-97

Perfect score: 66

Sequence: 1 KTEEISEVNLVAEF 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	77.3	82	PQ0438	Alzheimer's diseases
2	51	77.3	695	A49795	Alzheimer's diseases
3	51	77.3	695	A27485	Alzheimer's diseases
4	51	77.3	695	S00550	Alzheimer's diseases
5	51	77.3	770	QRHUA4	Alzheimer's diseases
6	45	68.2	747	JH0773	Alzheimer's diseases
7	43	65.2	1354	T13930	tripeptidyl-peptid
8	39	59.1	1127	D70671	pyruvate carboxyla
9	38.5	58.3	587	T48582	auxin-regulated pr
10	38	57.6	455	S50725	hypothetical prote
11	38	57.6	505	E95246	hypothetical prote
12	38	57.6	505	B98111	4-alpha-glucanotra
13	37	56.1	172	B83139	hypothetical prote
14	37	56.1	198	G97991	hypothetical prote
15	37	56.1	225	E97244	coltUC-like protein
16	37	56.1	335	A24785	hypothetical prote
17	37	56.1	366	B87446	hypothetical prote
18	37	56.1	867	T05389	hypothetical prote
19	37	56.1	1272	C90593	biopolymer transpo
20	37	56.1	1290	G64630	hypothetical prote
21	36	54.5	136	C81436	glycerophosphoryl
22	36	54.5	144	H70239	30K protein - toma
23	36	54.5	237	S73602	hypothetical prote
24	36	54.5	264	WMBVL2	methyl-accepting c
25	36	54.5	274	B96991	hypothetical prote
26	36	54.5	316	T23930	hypothetical prote
27	36	54.5	556	S75873	hypothetical prote
28	36	54.5	572	S72249	trithorax protein
29	36	54.5	600	T39516	threonine ammonia-

30	36	54.5	954	2	H97100	DNA gyrase A chain
31	36	54.5	967	2	JH0667	phosphoenolpyruvat
32	36	54.5	1047	2	T16203	hypothetical prote
33	36	54.5	1291	2	S44983	vacuolating cyto
34	35	53.0	206	2	AC1527	hypothetical prote
35	35	53.0	206	2	AI1169	hypothetical prote
36	35	53.0	270	2	AG0036	conserved hypothet
37	35	53.0	297	2	AC1706	hypothetical prote
38	35	53.0	297	2	AD1335	hypothetical prote
39	35	53.0	425	2	A71639	serine-tRNA ligase
40	35	53.0	425	2	H97851	55 kDa B regulator
41	35	53.0	512	2	G96555	protein phosphatas
42	35	53.0	513	2	S55889	nitrogenase (bc 1,
43	35	53.0	521	2	S27475	hypothetical prote
44	35	53.0	650	2	T22002	CHS5 protein - yea
45	35	53.0	671	2	S53407	

ALIGNMENTS

RESULT 1

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; MUID:93075180; PMID:1445331

A:Accession: PQ0438

A:Molecule type: DNA

A:Residues: 1-82 <DAY>

A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079; PMID:1656157

A:Accession: C60045

A:Molecule type: mRNA

A:Residues: 12-68 <JOH>

A:Cross-references: EMBL:X56129

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 77.3%; Score 51; DB 2; Length 82;

Best Local Similarity 78.6%; Pred. No. 0.025;

Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14

||||||| : |||

Db 7 KTEEISEVKMDAEF 20

RESULT 2

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A49795

R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports

A:Reference number: A49795; MUID:91273117; PMID:1905108

A:Accession: A49795

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing

Query Match 77.3%; Score 51; DB 1; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

RESULT 3
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sakaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
A:Reference number: A27485; MUID:88106489; PMID:332280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 77.3%; Score 51; DB 2; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.28; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

RESULT 4
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988

Query Match 77.3%; Score 51; DB 2; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

RESULT 5
QRH04
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA inh
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascu
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A3486; I39452; I39451; I39453; I59562;
4668; A28583; A29303; A08003; J00038; S06121; A60355; A59011; A38384; S29076; S38252;
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A:Note: alternative splice form APP(695)
R:La Faurie, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: Protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 77.3%; Score 51; DB 2; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:gl78863; PIDN:AAA51768.1; PID:gl78865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.F.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PREL>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Toshikari, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:gl78613; PIDN:AAB59502.1; PID:gl78616
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:gl78608; PIDN:AAB59501.1; PID:gl78615
R:Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:gl78618; PIDN:AAA51727.1; PID:gl78620
A:Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:Q236720; PIDN:AAB19991.1; PID:Q236721
R:Ramino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45136; NID:Q257379; PIDN:AAB23646.1; PID:Q257380
A:Experimental source: familial Alzheimer disease family Lit
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A:Reference number: A03134; MUID:87144572; PMID:2881207

A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:Q28525; PIDN:CAA68374.1; PID:Q28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:gl78539; PIDN:AAA51729.1; PID:gl78540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:gl78706; PIDN:AAA35540.1; PID:gl78707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M15532; NID:gl77957; PIDN:AAA51564.1; PID:gl77958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:Q28817; PIDN:CAA30042.1; PID:Q2929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:Q28720; PIDN:CAA30050.1; PID:Q28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inh
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:Q28816; PIDN:CAA30041.1; PID:Q929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain
A:Reference number: A31087; MUID:98124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAT>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A>Note: The authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 61
A>Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.
Query Match 77.3%; Score 51; DB 1; Length 770;
Best Local Similarity 78.6%; Pred. No. 0.32;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 KTEISEVNLVAEF 14
||||||| : |||
Db 662 KTEISEVNMDAEF 675
RESULT 6
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
C:Okada, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 68.2%; Score 45; DB 2; Length 747;
Best Local Similarity 64.3%; Pred. No. 4;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KTEISEVNLVAEF 14
||||||| : |||
Db 639 KTEISEVNMDSY 652
RESULT 7
T13930
tripeptidyl-peptidase II (EC 3.4.14.10) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13930
R:Krenn, S.C.P.; Tomkinson, B.; Taghert, P.H.
J. Biol. Chem. 273, 19173-19182, 1998
A:Title: Characterization and cloning of tripeptidyl peptidase II from the fruit fly, D
A:Reference number: Z17814; MUID:98334655; PMID:9668104
A:Accession: T13930
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-1354 <REN>
A:Cross-references: EMBL:AF035251; NID:g3387807; PID:g3387808; PIDN:AAC28563.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0020370
A:Map position: 2
C:Keywords: dipeptidylpeptide hydrolase

Query Match 65.2%; Score 43; DB 2; Length 1354;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 REISEVNLVAEF 14
||||| |||||
Db 929 ERISEANLVASF 940

RESULT 8

D70671
Pyruvate carboxylase (EC 6.4.1.1) - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2002
C:Accession: D70671; S73055
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70671
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1127 <COL>
A:Cross-references: GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05410.1; PID:g16948
A:Experimental source: strain H37RV
R:Smith, D.R.; Robinson, K.
submitted to the EMBL Data Library, September 1994
A:Description: Mycobacterium tuberculosis cosmid tbc2.
A:Reference number: S73053
A:Accession: S73055
A:Molecule type: DNA
A:Residues: 1-353, 'TRAGSARCDPPAVPVSAWTAAPTWRNPVLRHAGQADLS', 396-1115, 'EWRAETCWWV' <
A:Cross-references: EMBL:U00024; NID:g560506; PIDN:AAA50948.1; PID:g560527
C:Genetics:
A:Gene: pca; pyc
A:Start codon: GTG
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
C:Keywords: biotin binding; ligase; mitochondrion
F:4-457/Domain: biotin carboxylase homology <BCH>
F:1055-1127/Domain: lipoyl/biotin-binding homology <LPB>
F:1093/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 59.1%; Score 39; DB 2; Length 1127;
Best Local Similarity 72.7%; Pred. No. 84;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TEEISEVNLVA 12
||||| : |||
Db 300 TEEITDVLVA 310

RESULT 9

T48582
auxin-regulated protein GH3 homolog T31B5.170 - Arabidopsis thaliana
N:Alternate names: protein T31B5.170
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Jul-2001
C:Accession: T48582
R:Beyan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Banco
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24490
A:Accession: T48582
A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-587 <BEV>

A:Cross-references: EMBL:AL163491

A:Experimental source: EMBL:AL163491

C:Genetics:

A:Map position: 5

A:Introns: 97/2; 131/2; 178/2; 400/1

A:Note: T31B5.170

C:Superfamily: soybean auxin-regulated protein GH3

Query Match 58.3%; Score 38.5; DB 2; Length 587;

Best Local Similarity 58.8%; Pred. No. 50;

Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 1 KTEE---ISEVNLVAF 14

DB 562 KTEEAVKILEANVVSF 578

RESULT 10

S50725

hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein NI346

C:Species: Saccharomyces cerevisiae

C:Date: 23-Aug-1995 #sequence_revision 19-Jan-1996 #text_change 19-Apr-2002

C:Accession: S50725; S63163; S49863

R:Jonniaux, J.L.; Coster, F.; Purnelle, B.; Goffeau, A.

Yeast 10, 1639-1645, 1994

A:Title: A 21.7 kb DNA segment on the left arm of yeast chromosome XIV carries WHI3, GCR

A:Reference number: S50712; MUID:95242839; PMID:7725799

A:Accession: S50725

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-455 <JON>

A:Cross-references: EMBL:X78898; NID:9600045; PIDN:CAA55502.1; PID:g600059

R:Coster, F.; Jonniaux, J.L.; Goffeau, A.; Purnelle, B.; Van Dyck, L.

Submitted to the Protein Sequence Database, April 1996

A:Reference number: S63151

A:Accession: S63163

A:Molecule type: DNA

A:Residues: 1-455 <COS>

A:Cross-references: EMBL:Z71482; NID:gl302206; PID:e239612; PID:gl302207; MIPS:YNL206c

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:RTT106

A:Cross-references: SGD:S0005150

A:Map position: 14L

Query Match 57.6%; Score 38; DB 2; Length 455;

Best Local Similarity 63.6%; Pred. No. 46;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLV 11

DB 63 KTEEISENTI 73

RESULT 11

E95246

4-alpha-glucanotransferase [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C:Accession: E95246

R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: E95246

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-505 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK76166.1; PID:gl4973618; GSPDB:GN00164; TIGR:

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP2107

Query Match 57.6%; Score 38; DB 2; Length 505;

Best Local Similarity 54.5%; Pred. No. 52;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 EISEVNLVAE 13

DB 332 EELGELNIIAE 342

RESULT 12

B98111

4-alpha-glucanotransferase (EC 2.4.1.25) [imported] - Streptococcus pneumoniae (strain

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

C:Accession: B98111

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: B98111

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-505 <KUR>

A:Cross-references: GB:AE007317; PIDN:AAL00719.1; PID:gl5459613; GSPDB:GN00174

C:Genetics:

A:Gene: malM

C:Keywords: glycosyltransferase, hexosyltransferase

Query Match 57.6%; Score 38; DB 2; Length 505;

Best Local Similarity 54.5%; Pred. No. 52;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 EISEVNLVAE 13

DB 332 EELGELNIIAE 342

RESULT 13

B83139

hypothetical protein PA4066 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83139

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: B83139

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <STO>

A:Cross-references: GB:AE004822; GB:AE004091; NID:9950250; PIDN:AAC07453.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4066

Query Match 56.1%; Score 37; DB 2; Length 172;

Best Local Similarity 72.7%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 EISEVNLVAE 14

IIIIIIIIII

```

Db      89 EISEAGLVTEF 99

RESULT 14
G97991
hypothetical protein spr0959 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: G97991
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: G97991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <KUR>
A:Cross-references: GB:AF007317; PIDN:AAK9763.1; PID:gl5458570; GSPDB:GN00174
C:Genetics:
A:Gene: spr0959

Query Match          56.1%; Score 37; DB 2; Length 198;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      3 BEISEVNLVAE 13
      |::|::|::|
Db      64 EKISEINLMIE 74

RESULT 15
E97244
cotJC-like protein (GS80 family) [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: E97244
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97244
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <KUR>
A:Cross-references: GB:AF001437; PIDN:AAK80744.1; PID:gl5025840; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2800

Query Match          56.1%; Score 37; DB 2; Length 225;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TEEISEVNLVAE 13
      |::|::|::|
Db      65 TEELSHMEIVAE 76

Search completed: November 18, 2002, 12:54:08
Job time : 18.4348 secs

```

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:49:38 ; Search time 9.13043 seconds
(without alignments)
63.597 Million cell updates/sec

Title: US-09-724-571-97
Perfect score: 66
Sequence: 1 KTEEISEVNLVAEF 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	77.3	751	1 A4_SAISC	Q95241 saimiri sci
2	51	77.3	770	1 A4_HUMAN	P05067 homo sapien
3	51	77.3	770	1 A4_MOUSE	P12023 mus musculus
4	51	77.3	770	1 A4_RAT	P08592 rattus norv
5	38	57.6	455	1 YNU6_YEAST	P40161 saccharomyc
6	38	57.6	505	1 MALQ_STREP	P29851 streptococc
7	37	56.1	366	1 QUEA_CAUCR	Q9A7Y2 caulobacter
8	37	56.1	1290	1 VACA_HELPH	P55981 helicobacte
9	36	54.5	237	1 Y385_MYCPN	P75212 mycoplasma
10	36	54.5	264	1 MOVPT_TOML2	P29800 tomato mosa
11	36	54.5	309	1 FSTL_FLABI	P52838 flavaria bi
12	36	54.5	967	1 CAP2_MAIZE	P51059 zea mays (m
13	36	54.5	1291	1 VACA_HELPH	Q48258 helicobacte
14	35	53.0	425	1 SYS_RICPR	Q9C9G5 rickettsia
15	35	53.0	521	1 NIFK_AZOB	P25314 azospirillu
16	35	53.0	632	1 KU70_CHICK	Q93257 gallus gall
17	35	53.0	671	1 CHS5_YEAST	Q12114 saccharomyc
18	35	53.0	802	1 PAC_ARTVI	P31956 arthrobacte
19	35	53.0	802	1 PAC_BACME	Q60136 bacillus me
20	35	53.0	1178	1 PVC_HUMAN	P14928 homo sapien
21	35	53.0	1178	1 PVC_MOUSE	Q05920 mus musculus
22	35	53.0	1178	1 PVC_RAT	P52873 rattus norv
23	35	53.0	1562	1 YH81_YEAST	Q04781 saccharomyc
24	34	51.5	174	1 WRB_HUMAN	Q00258 homo sapien
25	34	51.5	216	1 RGSB_ECOLI	P14374 escherichia
26	34	51.5	216	1 RGSB_SALII	Q56127 salmonella
27	34	51.5	216	1 RGSB_SALII	P58663 salmonella
28	34	51.5	219	1 GSH2_PASMO	P57863 pasteurella
29	34	51.5	351	1 FLIC_SERMA	P13713 serratia ma
30	34	51.5	351	1 HRCFA_FUSNN	Q8rh08 fusobacteri
31	34	51.5	396	1 RL4A_XENLA	P08429 xenopus lae
32	34	51.5	396	1 RL4B_XENLA	P02385 xenopus lae
33	34	51.5	456	1 PUR8_ECOLI	P25739 escherichia

34 34 51.5 508 1 CC37_CANAL
35 34 51.5 540 1 BB61_RABIT
36 34 51.5 717 1 ECHP_MOUSE
37 34 51.5 721 1 ECHP_RAT
38 34 51.5 737 1 YMA2_YEAST
39 34 51.5 967 1 CAP1_FLAPR
40 34 51.5 1183 1 CNA_STAAU
41 34 51.5 1679 1 YIO9_YEAST
42 33.5 50.8 304 1 Y050_UREPA
43 33.5 50.8 808 1 YU08_CAEEL
44 33 50.0 151 1 MUP8_MOUSE
45 33 50.0 155 1 PR2_PHAVU

Q8xle6 candida alb
Q05004 oryctolagus
Q9dbm2 mus musculu
P07896 rattus norv
Q04263 saccharomyc
Q01647 flavaria pr
Q53654 staphylococ
P04057 saccharomyc
Q9pr95 ureaplasma
P34402 caenorhabdi
P04938 mus musculu
P25986 phaseolus v

ALIGNMENTS

RESULT 1

A4_SAISC
ID A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE amyloid protein (Beta-APP) (A-beta)].
GN APP
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
RX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=85321114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: S81024; AAD14347.1; -
CC HSSP: P05067; IAAP.
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR001255; Beta-APP.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC Pfam: PF02177; A4_EXTRA; 1.
CC Pfam: PF03494; Beta-APP; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC PRINTS: PR00759; BASICPTASE.
CC ProDom: PD000222; Kunitz_BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.

```

DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84899 MW; 6C3E431089569049 CRC64;

Query Match 77.3%; Score 51; DB 1; Length 751;
Best Local Similarity 78.6%; Pred. No. 0.15;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
| | | | | | | : | | |
DB 643 KTEEISEVKMDAEF 656

RESULT 2
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011.
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II).
DE (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;

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RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [6]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [7]
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=2893574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
RP SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RP SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [10]
RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [11]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RP SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with

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RT the Kunitz domain is protease nexin-II.";
RL Nature 341:144-147(1989).
RN [14]
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90011252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor.";
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RP COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O).";
RL Nature 362:75-79(1993).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=9921582; PubMed=10201399;
RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
RN [18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031498; PubMed=1718421;
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamarek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein.";
RL Biochemistry 30:10467-10478(1991).
RN [19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RL Biochemistry 33:7788-7796(1994).
RN [20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment.";
RL Biochemistry 35:16094-16104(1996).
RN [21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
RN [22]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RL J. Struct. Biol. 130:142-152(2000).
RN [23]
RP STRUCTURE BY NMR OF 681-706.

RX MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RT water.";
RL J. Struct. Biol. 130:130-141(2000).
RN [24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE=88296437; PubMed=2900137;
RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";
RN [25]
RP QUERY MATCH 77.3%; Score 51; DB 1; Length 770;
RX Best Local Similarity 78.6%; Pred. NO. 0.16;
RN Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 KTEISEVNLVAEF 14
DB 662 KTEISEVMDAEF 575
ID A4_MOUSE STANDARD; PRT; 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).

DR Pfam; PF02117; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT FT HOMOLOG.
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT SITE 291 341
FT DISULFID 300 324
FT DISULFID 306 337
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPLIC 289 289
FT VARSPLIC 290 364
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BBD2929A7 CRC64;

Query Match 77.3%; Score 51; DB 1; Length 770;
Best Local Similarity 78.6%; Pred. No. 0.16;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
| | | | | | | | | | | | | | | |
DB 662 KTEISEVKMDAEF 675

RESULT 5
YNU6_YEAST STANDARD; PRT; 455 AA.
AC P40161;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 51.6 kDa protein in SSB2-SPX18 intergenic region.
GN YNL206C OR N1346.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / FY1679;
RX MEDLINE=95242839; PubMed=7725799;
RA Jonniaux J.-L., Coster F., Purnelle B., Goffeau A.;
RT "A 21.7 kb DNA segment on the left arm of yeast chromosome XIV
RT carries WHI3, GCR2, SPX18, SPX19, an homologue to the heat shock gene
RT SSB1 and 8 new open reading frames of unknown function."
RL Yeast 10:1639-1645(1994).
CC -! SIMILARITY: SOME, TO DROSOPHILA AND MAMMALIAN SINGLE-STRAND
CC RECOGNITION PROTEINS (SSRP).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; X78898; CAA55502.1; -.
DR EMBL; Z71482; CAA96106.1; -.
DR SGD; S0005150; YNL206C.
KW Hypothetical protein.
SQ SEQUENCE 455 AA; 51621 MW; 79CACAC659A7F4F4D CRC64;

Query Match 57.6%; Score 38; DB 1; Length 455;
Best Local Similarity 63.6%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEISEVNLV 11
| | | | | | | | | | | |
DB 63 KTEISEVTNI 73

RESULT 6
MALQ_STRPN STANDARD; PRT; 505 AA.
AC P29851.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
DE (Disproportionating enzyme) (D-enzyme).
DE MALQ OR MAM OR SP2107.
GN Streptococcus pneumoniae.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129347; PubMed=6297760;
RA Lacks S.A., Dunn J.J., Greenberg B.;
RT "Identification of base mismatches recognized by the
RT heteroduplex-DNA-repair system of Streptococcus pneumoniae."
RL Cell 31:327-336(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holczapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae".
RL Science 293:498-506(2001).
CC -! CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan
CC to a new 4-position in an acceptor, which may be glucose or (1,4)-
CC alpha-D-glucan.
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC

DR EMBL; J01796; AAA26923.1; -.
DR EMBL; AE007499; AAK76166.1; -.
DR HSSP; O87172; 1CWY.
DR TIGR; SP2107; -.
DR InterPro; IPR003385; 4A_gluconotrans.
DR Pfam; PF02446; 4A_gluconotrans; 1.
DR TIGRFAMs; TIGR00217; malQ; 1.
KW Transferase; Glycosyltransferase; Carbohydrate metabolism;

Mon Nov 18 17:35:38 2002

```
KW Complete proteome.
SQ SEQUENCE 505 AA; 58076 MW; D4529A00A6D01A5 CRC64;

Query Match      57.6%; Score 38; DB 1; Length 505;
Best Local Similarity 54.5%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 REISEVNLVAE 13
   ||:|:|:|
Db 332 EEELGELNIIAE 342

RESULT 7
QUEA_CAUCR
ID QUEA_CAUCR STANDARD; PRT; 366 AA.
AC Q9A7Y2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine:trna ribosyltransferase-isomerase (EC 5.-.-.-)
DE (Queuosine biosynthesis protein queA).
DE QUEA OR CC1587.
GN Caulobacter crescentus.
OS Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Nieman W.C., Feldblyum T.V., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermoleva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- FUNCTION: Synthesizes oQ from preO1 in a single S-
CC adenosylmethionine-requiring step. The ribosyl moiety of Adomet is
CC transferred and isomerized to the epoxycyclopentane residue of oQ
CC (By similarity).
CC -!- PATHWAY: Queuosine biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE QUEA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005833; AAK23566.1; -
CC TIGR; CC1587; -
CC InterPro; IPR003699; Queuosine_synth.
CC Pfam; PF02547; Queuosine_synth; 1.
CC TIGRFAMs; TIGR00113; queA; 1.
CC Queuosine biosynthesis; Transferase; Isomerase; Complete proteome.
SQ SEQUENCE 366 AA; 39817 MW; A40DBE37E70C7C3 CRC64;

Query Match      56.1%; Score 37; DB 1; Length 366;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
   ||:|:|:|
Db 235 KTEVSEHRMAEY 248

RESULT 8
QUEA_CAUCR
ID QUEA_CAUCR STANDARD; PRT; 366 AA.
AC Q9A7Y2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine:trna ribosyltransferase-isomerase (EC 5.-.-.-)
DE (Queuosine biosynthesis protein queA).
DE QUEA OR CC1587.
GN Caulobacter crescentus.
OS Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Nieman W.C., Feldblyum T.V., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermoleva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA "Complete genome sequence of Caulobacter crescentus.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- FUNCTION: Synthesizes oQ from preO1 in a single S-
CC adenosylmethionine-requiring step. The ribosyl moiety of Adomet is
CC transferred and isomerized to the epoxycyclopentane residue of oQ
CC (By similarity).
CC -!- PATHWAY: Queuosine biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE QUEA FAMILY.
CC
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CC
CC EMBL; AF005833; AAK23566.1; -
CC TIGR; CC1587; -
CC InterPro; IPR003699; Queuosine_synth.
CC Pfam; PF02547; Queuosine_synth; 1.
CC TIGRFAMs; TIGR00113; queA; 1.
CC Queuosine biosynthesis; Transferase; Isomerase; Complete proteome.
SQ SEQUENCE 366 AA; 39817 MW; A40DBE37E70C7C3 CRC64;

Query Match      56.1%; Score 37; DB 1; Length 366;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
   ||:|:|:|
Db 235 KTEVSEHRMAEY 248

RESULT 9
Y385_MYCPN
ID Y385_MYCPN STANDARD; PRT; 237 AA.
AC P75212;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG385 homolog (H03_orf237).
DE MPN566 OR MP276.
GN Mycoplasma pneumoniae.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=21104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RA "The complete genome sequence of the gastric pathogen Helicobacter
RA pylori.";
RT Nature 388:539-547(1997).
RL -!- FUNCTION: INDUCES VACUOLATION OF EUKARYOTIC CELLS. CAUSES
CC ULCERATION AND GASTRIC LESIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
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CC
CC EMBL; AE000598; AAD07935.1; -
CC TIGR; HP0887; -
CC InterPro; IPR003842; Vaca.
CC Pfam; PF02691; Vaca; 1.
CC Cycotoxin; Toxin; Signal; Complete proteome.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 ? VACUOLATING CYTOTOXIN.
FT PROPEP ? 1290 POTENTIAL.
SQ SEQUENCE 1290 AA; 139312 MW; F48B23513447A1AC CRC64;

Query Match      56.1%; Score 37; DB 1; Length 1290;
Best Local Similarity 53.8%; Pred. No. 98;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEEISEVNLVAEF 14
   ||:|:|:|
Db 746 TNSISVNLIEQF 758

RESULT 9
Y385_MYCPN
ID Y385_MYCPN STANDARD; PRT; 237 AA.
AC P75212;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG385 homolog (H03_orf237).
DE MPN566 OR MP276.
GN Mycoplasma pneumoniae.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=21104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RA "The complete genome sequence of the gastric pathogen Helicobacter
RA pylori.";
RT Nature 388:539-547(1997).
RL -!- FUNCTION: INDUCES VACUOLATION OF EUKARYOTIC CELLS. CAUSES
CC ULCERATION AND GASTRIC LESIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC
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CC
CC EMBL; AE000598; AAD07935.1; -
CC TIGR; HP0887; -
CC InterPro; IPR003842; Vaca.
CC Pfam; PF02691; Vaca; 1.
CC Cycotoxin; Toxin; Signal; Complete proteome.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 ? VACUOLATING CYTOTOXIN.
FT PROPEP ? 1290 POTENTIAL.
SQ SEQUENCE 1290 AA; 139312 MW; F48B23513447A1AC CRC64;
```

```
RC STRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirk1 E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
RC -!- SIMILARITY: TO GLYCROPHOSPHORYL DIESTER PHOSPHODIESTERASES (EC
CC 3.1.4.46).
CC -!- SIMILARITY: M.GENITALIUM MG293.
CC -----
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CC -----
DR EMBL; AE000027; AAB95924.1; -.
DR InterPro; IPR004129; GPPD.
DR Pfam; PF03009; GPPD; 1.
KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 237 AA; 27716 MW; D0EE0A302F07F2C8 CRC64;
Query Match 54.5%; Score 36; DB 1; Length 237;
Best Local Similarity 54.5%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KTEEISEVNLV 11
DB 60 KTHKLSIDINLV 70
RESULT 10
MOV_P_TOML2
ID MOV_P_TOML2 STANDARD; PRT; 264 AA.
AC P29800;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Movement protein (Cell-to-cell transport protein) (30 kDa protein).
GN MP.
OS Tomato mosaic virus (strain LII) (TOMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=31747;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92113565; PubMed=1730937;
RA Calder V.L., Palukaitis P.;
RT "Nucleotide sequence analysis of the movement genes of resistance
RT breaking strains of tomato mosaic virus.";
RL J. Gen. Virol. 73:165-168(1992).
CC -!- FUNCTION: Involved in transport of the virus from the initially
CC infected cells to adjacent cells, possibly by modifying the
CC function of the plasmodesmata. Also influences local lesion
CC development. Binds to RNA and single-stranded DNA.
CC -!- SIMILARITY: BELONGS TO THE TOBAMOVIRUSES MOVEMENT PROTEIN FAMILY.
CC PIR: J01457; WMBVL2.
DR InterPro; IPR001022; TMV_movement.
DR Pfam; PF01107; Tobamo_MP; 1.
DR PRINTS; PR00964; MOVEMENT.
KW DNA-binding; RNA-binding; Transport.
SQ SEQUENCE 264 AA; 29396 MW; 4737590A4EB8903B CRC64;
Query Match 54.5%; Score 36; DB 1; Length 264;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KTEEISEVNLV 11
DB 46 KNESEVNL 56
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RESULT 11
FSTL_FLABI STANDARD; PRT; 309 AA.
ID FSTL_FLABI STANDARD; PRT; 309 AA.
AC P52838;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Flavonol sulfotransferase-like (EC 2.8.2.-).
OS Flaveria bidentis.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
CC Heleniae; Flaveria.
OX NCBI_TaxID=4224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95232186; PubMed=7716232;
RA Ananvoranich S., Gulick P., Ibrahim R.K.;
RT "Flavonol sulfotransferase-like cDNA clone from Flaveria bidentis.";
RL Plant Physiol. 107:1019-1020(1995).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE PLANT SULFOTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL; U10277; AAA87399.1; -.
DR HSP; P50224; ICJM.
DR InterPro; IPR000863; Sulfotransferase.
DR Pfam; PF06885; Sulfotransfer; 1.
DR ProDom; PD001218; Sulfotransferase; 1.
KW Transferase.
FT BINDING 138 153 PAPS-BINING SITE (BY SIMILARITY).
SQ SEQUENCE 309 AA; 35917 MW; 598A9C9EFBB75303 CRC64;
Query Match 54.5%; Score 36; DB 1; Length 309;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 KTEEISEVNLVAEF 14
DB 211 KSEPISNVKKLAEF 224
RESULT 12
CAP2_MAIZE
ID CAP2_MAIZE STANDARD; PRT; 967 AA.
AC P51059;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Phosphoenolpyruvate carboxylase 2 (EC 4.1.1.31) (PEPCASE).
GN PEP4 OR PEP.
OS Zea mays (Maize).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
CC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. H84; TISSUE=Root;
RX MEDLINE=93054411; PubMed=1429504;
RA Kawamura T., Shigesada K., Toh H., Okumura S., Yanagisawa S.,
RA Izui K.;
RT "Molecular evolution of phosphoenolpyruvate carboxylase for C4
RT photosynthesis in maize: comparison of its cDNA sequence with a newly
RT isolated cDNA encoding an isozyme involved in the anaplerotic
```

RT function.";
RL J. Biochem. 112:147-154(1992).
CC -!- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID
CC SOURCE FOR THE TRICARBOXYLIC ACID CYCLE.
CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
CC phosphoenolpyruvate + CO(2).
CC -!- ENZYME REGULATION: BY LIGHT-REVERSIBLE PHOSPHORYLATION (BY
CC SIMILARITY).
CC -!- PATHWAY: TRICARBOXYLIC ACID CYCLE. THIS ISOZYME IS INVOLVED IN
CC C3 PHOTOSYNTHESIS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
CC -----
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CC -----
DR EMBL; X61489; CAA43709.1; -.
DR HSSP; P00864; 1FYI.
DR MaizeDB; 30066; -.
DR InterPro; IPR001449; PEPCase.
DR Pfam; PF00311; PEPCase; 1.
DR PRINTS; PR00150; PEPCARBLASE.
DR PROSITE; PS00393; PEPCASE-2; 1.
DR PROSITE; PS00781; PEPCASE-1; 1.
KW Lyase; Carbon dioxide fixation; Allosteric enzyme; Multigene family;
KW Tricarboxylic acid cycle; Phosphorylation; Photosynthesis.
FT MOD_RES 13 13 PHOSPHORYLATION (BY SIMILARITY).
FT ACT_SITE 174 174 BY SIMILARITY.
FT ACT_SITE 602 602 BY SIMILARITY.
SQ SEQUENCE 967 AA; 109998 MW; 7034A2AD5521645B CRC64;

Query Match 54.5%; Score 36; DB 1; Length 967;
Best Local Similarity 52.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 4; Gaps 1;

Qy 1 KTEEISEV----NLVAE 13
Db 503 KTEEISDVLDTFFHVAE 519
|||||||:| :|:|

RESULT 13
VAC4_HELPY
ID VAC4_HELPY STANDARD; PRT; 1291 AA.
AC Q48258;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Vacuolating cytotoxin precursor.
GN VACA.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=185-44;
RX MEDLINE=94335650; PubMed=8057855;
RA Haas R., Schmitt W.;
RT "Genetic analysis of the Helicobacter pylori vacuolating cytotoxin:
RT structural similarities with the Iga protease type of exported
RT protein.";
RL Mol. Microbiol. 12:307-319(1994).
CC -!- FUNCTION: INDUCES VACUOLATION OF EUKARYOTIC CELLS. CAUSES
CC ULCEATION AND GASTRIC LESIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC -----
DR EMBL; Z26883; CAA81528.1; -.
DR InterPro; IPR003842; Vaca.
DR Pfam; PF02691; Vaca; 1.
KW Cytotoxin; Toxin; Signal.
FT SIGNAL 1 33
FT CHAIN 34 ? VACUOLATING CYTOTOXIN.
FT PROPEP ? 1291 POTENTIAL.
SQ SEQUENCE 1291 AA; 139635 MW; ECA56A61CAE36669 CRC64;

Query Match 54.5%; Score 36; DB 1; Length 1291;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TEEISEVNLVAEF 14
Db 746 TDSIANVNLIQEF 758
|:|:|:|:|

RESULT 14
SYS_RICPR
ID SYS_RICPR STANDARD; PRT; 425 AA.
AC Q9ZCG5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Seryl--trNA synthetase (EC 6.1.1.11) (Seryl--trNA ligase) (SerRS).
GN SERS OR Rp783.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-serine + trNA(Ser) = AMP + diphosphate
CC + L-seryl--trNA(Ser).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235273; CAA15209.1; -.
DR HSSP; P34945; 1SER.
DR InterPro; IPR002106; AARNA_ligaseII.
DR InterPro; IPR002314; trNA-synt_2b.
DR InterPro; IPR002317; trNA-synt_ser.
DR Pfam; PF00587; trNA-synt_2b; 1.
DR Pfam; PF02403; Seryl--trNA_N; 1.
DR PRINTS; PR00981; TRNASYNTHSER.
DR TIGREMS; TIGR00414; sers; 1.
DR PROSITE; PS50862; AA-TRNA_LIGASE_II; 1.
KW Aminoacyl--trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

Job time : 11.1304 secs

```
KW Complete proteome.
SQ SEQUENCE 425 AA; 48643 MW; 6977C5A5CAA30515 CRC64;

Query Match      53.0%; Score 35; DB 1; Length 425;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 TEEISEVNLVAE 13
   | | | | |
Db 228 TAEVSLNIVAD 239

RESULT 15
NIFK_AZOBR
ID NIFK_AZOBR STANDARD; PRT; 521 AA.
AC P25314;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)
DE (Nitrogenase component I) (Dinitrogenase).
GN NIFK
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Azospirillum.
OX NCBI_TaxID=192;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92370074; PubMed=1823284;
RA Passaglia L.M.P., Nunes C.P., Zaha A., Schrank I.S.;
RT "The nifHDK operon in the free-living nitrogen-fixing bacteria
RT Azospirillum brasilense sequentially comprises genes H, D, K, an 353
RT bp orf and gene v.";
RL Braz. J. Med. Biol. Res. 24:649-675(1991).
CC -!- FUNCTION: THE KEY ENZYMIC REACTIONS IN NITROGEN FIXATION ARE
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CC -!- CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 ATP
CC = 8 oxidized ferredoxin + 2 NH(3) + 16 ADP + 16 phosphate.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains that binds
CC 30-32 Fe, 2 Mo, and inorganic sulfur.
CC -!- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
CC -----
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CC -----
DR EMBL; M54344; AAB02344.1; -.
DR FIR; S27475; S27475.
DR HSSP; P07329; 3MIN.
DR InterPro; IPR000318; Nitrogense_Compl.
DR InterPro; IPR000510; Oxred_nitrogensel.
DR Pfam; PF00148; oxidored_nitro; 1.
DR TIGRFAMs; TIGR01286; nifK; 1.
DR PROSITE; PS00090; NITROGENASE_1_2; 1.
DR PROSITE; PS00699; NITROGENASE_1_1; 1.
DR Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
KW Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
SQ SEQUENCE 521 AA; 58216 MW; 4056110ED573DBA4 CRC64;

Query Match      53.0%; Score 35; DB 1; Length 521;
Best Local Similarity 61.5%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAE 13
   | | | | |
Db 55 KTEEYKEKNLPVE 67
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:50:24 ; Search time 29.8261 Seconds
(without alignments)
96.716 Million cell updates/sec

Title: US-09-724-571-97

Perfect score: 66

Sequence: 1 KTEEISEVNLVAEF 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	51	77.3	35	Q8WZ99	Q8WZ99 homo sapien
2	51	77.3	79	O35463	O35463 cricetus
3	51	77.3	82	Q16014	Q16014 homo sapien
4	51	77.3	82	Q16019	Q16019 homo sapien
5	51	77.3	82	Q16020	Q16020 homo sapien
6	51	77.3	82	Q16020	Q16020 homo sapien
7	51	77.3	607	Q99K32	Q99K32 mus musculu
8	51	77.3	695	Q95KN7	Q95KN7 macaca fasc
9	51	77.3	695	Q60496	Q60496 cavia sp. p
10	51	77.3	695	Q97487	Q97487 mus musculu
11	51	77.3	770	Q97UI0	Q97UI0 sus scrofa
12	50	75.8	534	Q93296	Q93296 gallus gall
13	50	75.8	569	Q9PVL1	Q9PVL1 gallus gall
14	50	75.8	695	Q9DGJ8	Q9DGJ8 gallus gall
15	50	75.8	751	Q9DGJ7	Q9DGJ7 gallus gall
16	45	68.2	658	Q8W0R6	Q8W0R6 sorghum bic

17	45	68.2	693	13	Q98SG0	Q98sg0 xenopus lae
18	45	68.2	747	13	Q91963	Q91963 xenopus. ap
19	43	65.2	1354	5	Q9V6251	O76251 drosophila
20	43	65.2	1354	5	Q9V6K1	O96K1 drosophila
21	42	63.6	699	13	Q57394	O57394 narke japon
22	40	60.6	497	16	Q8XHV6	O8xhv6 clostridium
23	39	59.1	228	1	Q9HH15	Q9hh15 methanosarc
24	39	59.1	695	13	Q98SP9	Q98sf9 xenopus lae
25	39	59.1	1124	2	Q50450	Q50450 mycobacteri
26	39	59.1	1127	16	P95127	P95127 mycobacteri
27	38.5	58.3	587	10	Q9LYU1	Q9lyu1 arabidopsis
28	38	57.6	371	2	O86250	O86250 helicobacte
29	38	57.6	608	17	Q8ZTJ3	Q8ztj3 pyrobaculum
30	38	57.6	829	2	Q9F9F8	Q9f9f8 helicobacte
31	38	57.6	1133	16	Q8RDW1	Q8rdw1 fusobacteri
32	37	56.1	152	2	Q8RRJ7	Q8rrj7 helicobacte
33	37	56.1	152	2	Q8RRF1	Q8rrf1 helicobacte
34	37	56.1	152	2	Q8RRE6	Q8rre6 helicobacte
35	37	56.1	152	2	Q8RRE1	Q8rre1 helicobacte
36	37	56.1	152	2	Q8RRD8	Q8rrd8 helicobacte
37	37	56.1	152	2	Q8RRD7	Q8rrd7 helicobacte
38	37	56.1	152	2	Q8RRC0	Q8rrc0 helicobacte
39	37	56.1	152	2	Q8RRB7	Q8rrb7 helicobacte
40	37	56.1	152	2	Q8RRB6	Q8rrb6 helicobacte
41	37	56.1	152	2	Q8RRB3	Q8rrb3 helicobacte
42	37	56.1	152	2	Q8RRB2	Q8rrb2 helicobacte
43	37	56.1	169	10	Q94KH1	Q94kh1 phaseolus v
44	37	56.1	172	16	Q9HWW2	Q9hww2 pseudomonas
45	37	56.1	186	16	Q9L267	Q9l267 streptomyce

ALIGNMENTS

RESULT 1

Q8WZ99 PRELIMINARY; PRT; 35 AA.

AC Q8WZ99;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Amyloid protein (Fragment).

GN APP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Wakutani Y., Ninomiya H., Iwata H., Tanaka S., Urakami K., Adachi Y.,

RA Wada-Isoe K., Yanagata K., Ohono K., Tsubuki S., Saigo T.,

RA Hashimoto T., Iwatsubo T., Nakashima K.;

RT "Novel missense mutation (D678N) of amyloid precursor protein gene in

RT a Japanese pedigree of familial Alzheimer's disease.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB066441; BAB1958.1; -

FT NON_TER

FT NON_TER

SQ SEQUENCE 35 AA; 4084 MW; 49D7D17289743B71 CRC64;

Query Match 77.3%; Score 51; DB 4; Length 35;
Best Local Similarity 78.6%; Pred. No. 0.021;

Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14

||||||| : |||

Db 7 KTEEISEVNLVAEF 20

RESULT 2

O35463

ID O35463 PRELIMINARY; PRT; 79 AA.

AC O35463;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Alzheimer's amyloid beta protein (Fragment).
 GN BETA APP.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB8608.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON_TER 1
 FT NON_TER 79
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 77.3%; Score 51; DB 11; Length 79;
 Best Local Similarity 78.6%; Pred. No. 0.049;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
 ||||| : |||
 DB 11 KTEISEVKMDAEF 24

RESULT 3
 Q16014
 ID Q16014 PRELIMINARY; PRT; 82 AA.
 AC Q16014;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Derman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S60721; AAB26263.2; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 77.3%; Score 51; DB 4; Length 82;
 Best Local Similarity 78.6%; Pred. No. 0.051;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
 . ||||| : |||
 DB 8 KTEISEVKMDAEF 21

RESULT 4
 Q16019
 ID Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Derman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61380; AAB26264.2; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 77.3%; Score 51; DB 4; Length 82;
 Best Local Similarity 78.6%; Pred. No. 0.051;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
 ||||| : |||
 DB 8 KTEISEVKMDAEF 21

RESULT 5
 Q16020
 ID Q16020 PRELIMINARY; PRT; 82 AA.
 AC Q16020;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Derman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61383; AAB26265.2; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 77.3%; Score 51; DB 4; Length 82;
 Best Local Similarity 78.6%; Pred. No. 0.051;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
 ||||| : |||
 DB 8 KTEISEVKMDAEF 21

RESULT 6
 P78438
 ID P78438 PRELIMINARY; PRT; 82 AA.
 AC P78438;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Amyloid protein (Beta-amyloid protein) (Fragment).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89392030; PubMed=2675837;
RX Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.,
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor."
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RN SEQUENCE OF 19-48 FROM N.A.
RP MEDLINE=87120329; PubMed=2949367;
RX Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.,
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus."
RL Science 235:880-884(1987).
RN [3]
RN SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=9303397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.,
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region."
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1;
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1;
DR EMBL; S45136; AAB23646.1;
DR HSSP; P05067; IBA4.
DR InterPro: IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9EA2B813A070E CRC64;

Query Match 77.3%; Score 51; DB 4; Length 82;
Best Local Similarity 78.6%; Pred. No. 0.051;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 7 KTEEISEVKMDAEF 20
||||| : |||
KTEEISEVNLVAEF 20
KTEEISEVKMDAEF 20

RESULT 7
Q99K32 PRELIMINARY; PRT; 507 AA.
ID Q99K32; (Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE Hypothetical 68.4 kDa protein (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1;
DR HSSP; P05067; 1AAP.
DR MGD; MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.

DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 58391 MW; BF802214CBA7D172 CRC64;

Query Match 77.3%; Score 51; DB 11; Length 607;
Best Local Similarity 78.6%; Pred. No. 0.41;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 499 KTEEISEVKMDAEF 512
||||| : |||
KTEEISEVNLVAEF 14
KTEEISEVKMDAEF 512

RESULT 8
Q95KN7 PRELIMINARY; PRT; 695 AA.
ID Q95KN7;
AC Q95KN7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Amyloid b-protein precursor.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease."
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1;
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; UNKNOWN_1.
DR PROSITE; PS00320; A4_INTRA; UNKNOWN_1.
FT SIGNAL 1
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 77.3%; Score 51; DB 6; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600
||||| : |||
KTEEISEVNLVAEF 14
KTEEISEVKMDAEF 600

RESULT 9
Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496
AC Q60496;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative amyloid precursor protein.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; IHA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 77.3%; Score 51; DB 11; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

RESULT 10
P97487
ID P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hippocampal amyloid protein.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Word L., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capeocchi M.,
RA Loring J.F., Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -.
DR EMBL; U82624; AAB40919.1; -.
DR HSSP; P05067; LMWP.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative amyloid precursor protein.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; IHA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 77.3%; Score 51; DB 11; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

RESULT 11
Q9TUI0
ID Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Amyloid precursor protein.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1; -.
DR HSSP; P05067; IAAp.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 77.3%; Score 51; DB 6; Length 770;
Best Local Similarity 78.6%; Pred. No. 0.53;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 662 KTEEISEVKMDAEF 675

RESULT 12
O93296
ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
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Query Match 77.3%; Score 51; DB 11; Length 695;
Best Local Similarity 78.6%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 587 KTEEISEVKMDAEF 600

RESULT 11
Q9TUI0
ID Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Amyloid precursor protein.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1; -.
DR HSSP; P05067; IAAp.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 77.3%; Score 51; DB 6; Length 770;
Best Local Similarity 78.6%; Pred. No. 0.53;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
DB 662 KTEEISEVKMDAEF 675

RESULT 12
O93296
ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
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RT "Increased production of amyloid precursor protein provides a
 RL substrate for caspase-3 in dying motoneurons.";
 J. Neurosci. 18:5869-5880(1998).
 DR EMBL; AF042098; AAC25052.1; -;
 DR HSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER
 SQ SEQUENCE 534 AA; 60597 MW; FB53BCC2E66D4C92 CRC64;

Query Match 75.8%; Score 50; DB 13; Length 534;
 Best Local Similarity 71.4%; Pred. No. 0.56; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTEISEVNLVAEF 14
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 Db 426 KTEEVSEVKMDAEF 439

RESULT 13

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
 AC Q9PVL1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Amyloid protein (Fragment).
 GN APP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Coulson E.J., Pallaga K., Beyreuther K., Masters C.L.;
 RT "What the evolution of the amyloid protein precursor supergene family
 RT tells us about its function.";
 RL Neurochem. Int. 0:0-0(2000).
 DR EMBL; AF030341; AAF12698.1; -;
 DR HSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 75.8%; Score 50; DB 13; Length 569;
 Best Local Similarity 71.4%; Pred. No. 0.6; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTEISEVNLVAEF 14
 ||||:||||: |||
 Db 462 KTEEVSEVKMDAEF 475

RESULT 14

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 AC Q9DGJ8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289218; AAG00593.1; -;
 DR HSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 75.8%; Score 50; DB 13; Length 695;
 Best Local Similarity 71.4%; Pred. No. 0.74; 2; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KTEISEVNLVAEF 14
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 Db 587 KTEEVSEVKMDAEF 600

RESULT 15

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.
 AC Q9DGJ7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289219; AAG00594.1; -;
 DR HSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 75.8%; Score 50; DB 13; Length 751;
 Best Local Similarity 71.4%; Pred. No. 0.8;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
 III:III : III
 Db 643 KTEEVSEVKMDAEF 656

Search completed: November 18, 2002, 12:53:33
 Job time : 29.8261 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:51:08 ; Search time 13.3913 Seconds
(without alignments)
30.760 Million cell updates/sec

Title: US-09-724-571-97
Perfect score: 66
Sequence: 1 KTEISEVNLVAF 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	59	89.4	30	2	US-08-659-984A-17
2	59	89.4	30	4	US-08-660-531-17
3	59	89.4	33	2	US-08-659-984A-16
4	59	89.4	33	4	US-08-660-531-16
5	59	89.4	42	2	US-08-659-984A-15
6	59	89.4	42	4	US-08-660-531-15
7	59	89.4	506	2	US-08-659-984A-21
8	59	89.4	506	4	US-08-660-531-21
9	59	89.4	506	4	US-09-054-334-4
10	59	89.4	695	4	US-09-548-372D-12
11	59	89.4	695	4	US-09-548-367D-12
12	59	89.4	697	4	US-09-548-372D-18
13	59	89.4	697	4	US-09-548-367D-18
14	51	77.3	58	1	US-08-371-930-25
15	51	77.3	58	5	PCT-US94-01712-25
16	51	77.3	152	6	5187133-4
17	51	77.3	162	6	5220013-4
18	51	77.3	162	6	5223482-4
19	51	77.3	264	1	US-07-990-893-5
20	51	77.3	487	1	US-08-462-859A-9
21	51	77.3	487	1	US-08-123-659A-9
22	51	77.3	487	1	US-08-464-247A-9
23	51	77.3	487	1	US-08-464-248A-9
24	51	77.3	492	1	US-08-462-859A-7
25	51	77.3	492	1	US-08-123-659A-7
26	51	77.3	492	1	US-08-464-247A-7
27	51	77.3	492	1	US-08-464-248A-7

28 51 77.3 1 US-08-371-930-23 Sequence 23, Appl
29 51 77.3 5 PCT-US94-01712-23 Sequence 23, Appl
30 51 77.3 656 5 PCT-US94-01712-23 Sequence 24, Appl
31 51 77.3 676 1 PCT-US94-01712-24 Sequence 24, Appl
32 51 77.3 694 1 US-08-339-152A-18 Sequence 18, Appl
33 51 77.3 694 2 US-08-007-998B-5 Sequence 5, Appl
34 51 77.3 694 2 US-08-689-276A-5 Sequence 5, Appl
35 51 77.3 695 1 US-08-371-930-27 Sequence 27, Appl
36 51 77.3 695 1 US-08-123-702-2 Sequence 2, Appl
37 51 77.3 695 1 US-08-339-152A-30 Sequence 30, Appl
38 51 77.3 695 2 US-08-104-165-1 Sequence 1, Appl
39 51 77.3 695 3 US-08-464-250-1 Sequence 1, Appl
40 51 77.3 695 4 US-08-464-250-1 Sequence 1, Appl
41 51 77.3 695 4 US-09-458-481B-4 Sequence 4, Appl
42 51 77.3 695 4 US-09-458-481B-5 Sequence 5, Appl
43 51 77.3 695 4 US-09-458-481B-6 Sequence 6, Appl
44 51 77.3 695 4 US-09-458-481B-7 Sequence 7, Appl
45 51 77.3 695 4 US-09-458-481B-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-659-984A-17
; Sequence 17, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-659-984A-17

Query Match 89.4%; Score 59; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 17 KTEEISEVNLDAEF 30

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-16

Query Match 89.4%; Score 59; DB 2; Length 33;
Best Local Similarity 92.9%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 8 KTEEISEVNLDAEF 21

US-08-660-531-16
Sequence 16, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-17

Query Match 89.4%; Score 59; DB 4; Length 30;
Best Local Similarity 92.9%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 17 KTEEISEVNLDAEF 30

US-08-659-984A-16
Sequence 16, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-16

Query Match 89.4%; Score 59; DB 4; Length 33;
Best Local Similarity 92.9%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 8 KTEEISEVNLDAEF 21

RESULT 5.
US-08-659-984A-15
Sequence 15, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-15

Query Match 89.4%; Score 59; DB 2; Length 42;
Best Local Similarity 92.9%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 17 KTEEISEVNLDAEF 30
RESULT 6
US-08-660-531-15
Sequence 15, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-15

Query Match 89.4%; Score 59; DB 4; Length 42;
Best Local Similarity 92.9%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 17 KTEEISEVNLDAEF 30

RESULT 7
US-08-659-984A-21
Sequence 21, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Ctr., 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/659,984A
 FILING DATE: 07-JUN-1996
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,152
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 506 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-659-984A-21

Query Match 89.4%; Score 59; DB 2; Length 506;
 Best Local Similarity 92.9%; Pred. No. 0.0056;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
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 Db 398 KTEEISEVNLDAEF 411

RESULT 8
 US-08-660-531-21
 Sequence 21, Application US/08660531
 Patent No. 6221645
 GENERAL INFORMATION:
 APPLICANT: Chrysler, Susanna M.S.
 APPLICANT: Sinha, Sukanto
 APPLICANT: Keim, Pamela S.
 APPLICANT: Anderson, John P.
 TITLE OF INVENTION: Beta-Secretase
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Ctr., 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/660,531
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/480,498
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002210US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 506 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-660-531-21
 Query Match 89.4%; Score 59; DB 4; Length 506;
 Best Local Similarity 92.9%; Pred. No. 0.0056;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
 |||||
 Db 398 KTEEISEVNLDAEF 411

RESULT 9
 US-09-054-334-4
 Sequence 4, Application US/09054334
 Patent No. 6329163
 GENERAL INFORMATION:
 APPLICANT: Anderson, John P.
 APPLICANT: Jacobson-Croak, Kirsten L.
 APPLICANT: Sinha, Sukanto
 TITLE OF INVENTION: Assays for Detecting Beta-Secretase
 TITLE OF INVENTION: Inhibition
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/054,334
 FILING DATE: 02-APR-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/485,152
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 015270-002820US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 506 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-054-334-4

Query Match 89.4%; Score 59; DB 4; Length 506;
 Best Local Similarity 92.9%; Pred. No. 0.0056;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14

Db 398 KTEISEVNLDAEF 411
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RESULT 10

US-09-548-372D-12
; Sequence 12, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-12

Query Match 89.4%; Score 59; DB 4; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.008;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
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Db 587 KTEISEVNLDAEF 600

RESULT 11

US-09-548-367D-12
; Sequence 12, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-12

Query Match 89.4%; Score 59; DB 4; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.008;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
|||||||

Db 587 KTEISEVNLDAEF 600

RESULT 12

US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-18

Query Match 89.4%; Score 59; DB 4; Length 697;
Best Local Similarity 92.9%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
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Db 587 KTEISEVNLDAEF 600

RESULT 13

US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 89.4%; Score 59; DB 4; Length 697;
Best Local Similarity 92.9%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
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Db 587 KTEISEVNLDAEF 600

Mon Nov 18 17:35:36 2002

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/019,208
; FILING DATE: February 18, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/154001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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PCT-US94-01712-25

Query Match 77.3%; Score 51; DB 5; Length 58;
Best Local Similarity 78.6%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
Db 37 KTEEISEVKMDAEF 50

Search completed: November 18, 2002, 12:54:35
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Query Match 77.3%; Score 51; DB 1; Length 58;
Best Local Similarity 78.6%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 KTEEISEVNLVAEF 14
Db 37 KTEEISEVKMDAEF 50
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RESULT 15
PCT-US94-01712-25
; Sequence 25, Application PC/TUS9401712
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:52:19 ; Search time 8.52174 Seconds
(without alignments)
24.743 Million cell updates/sec

Title: US-09-724-571-97

Perfect score: 66

Sequence: 1 KTEISEVNLVAEF 14

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Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubpa/PCIT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	59	89.4	30	10	US-09-896-139-9
3	59	89.4	30	10	US-09-895-843-9
4	59	89.4	32	10	US-09-896-874-4
5	59	89.4	32	10	US-09-896-139-4
6	59	89.4	32	10	US-09-895-843-4
7	59	89.4	33	10	US-09-896-874-6
8	59	89.4	33	10	US-09-896-139-6
9	59	89.4	33	10	US-09-895-843-6
10	59	89.4	695	10	US-09-794-927-12
11	59	89.4	695	10	US-09-795-847-12
12	59	89.4	695	10	US-09-794-743-12
13	59	89.4	695	10	US-09-794-748-12
14	59	89.4	695	10	US-09-794-925-12
15	59	89.4	695	10	US-09-681-442-12
16	59	89.4	697	10	US-09-794-927-18
17	59	89.4	697	10	US-09-795-847-18
18	59	89.4	697	10	US-09-794-743-18
19	59	89.4	697	10	US-09-794-748-18

20	59	89.4	697	10	US-09-794-925-18	Sequence 18, Appl
21	59	89.4	697	10	US-09-681-442-18	Sequence 18, Appl
22	51	77.3	695	10	US-09-794-927-10	Sequence 10, Appl
23	51	77.3	695	10	US-09-794-927-14	Sequence 14, Appl
24	51	77.3	695	10	US-09-795-847-10	Sequence 10, Appl
25	51	77.3	695	10	US-09-795-847-14	Sequence 14, Appl
26	51	77.3	695	10	US-09-794-743-10	Sequence 10, Appl
27	51	77.3	695	10	US-09-794-743-14	Sequence 14, Appl
28	51	77.3	695	10	US-09-794-748-10	Sequence 10, Appl
29	51	77.3	695	10	US-09-794-748-14	Sequence 14, Appl
30	51	77.3	695	10	US-09-794-925-10	Sequence 10, Appl
31	51	77.3	695	10	US-09-794-925-14	Sequence 14, Appl
32	51	77.3	695	10	US-09-681-442-10	Sequence 10, Appl
33	51	77.3	695	10	US-09-681-442-14	Sequence 14, Appl
34	51	77.3	695	10	US-09-149-718-2	Sequence 2, Appl
35	51	77.3	697	10	US-09-794-927-16	Sequence 16, Appl
36	51	77.3	697	10	US-09-794-927-20	Sequence 20, Appl
37	51	77.3	697	10	US-09-795-847-16	Sequence 16, Appl
38	51	77.3	697	10	US-09-795-847-20	Sequence 20, Appl
39	51	77.3	697	10	US-09-794-743-16	Sequence 16, Appl
40	51	77.3	697	10	US-09-794-743-20	Sequence 20, Appl
41	51	77.3	697	10	US-09-794-748-16	Sequence 16, Appl
42	51	77.3	697	10	US-09-794-748-20	Sequence 20, Appl
43	51	77.3	697	10	US-09-794-925-16	Sequence 16, Appl
44	51	77.3	697	10	US-09-794-925-20	Sequence 20, Appl
45	51	77.3	697	10	US-09-681-442-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-896-874-9
; Sequence 9, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40US01
; CURRENT APPLICATION NUMBER: US/09/896.874
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-9

Query Match 89.4%; Score 59; DB 10; Length 30;
Best Local Similarity 92.9%; Pred. No. 8.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14

Db 17 KTEISEVNLDAEF 30

RESULT 2

US-09-896-139-9
; Sequence 9, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy

Mon Nov 18 17:35:37 2002

APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mailleard, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: TenBrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.25USU4
CURRENT APPLICATION NUMBER: US/09/896,139
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/268,497
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/279,779
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/295,589
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-139-9

Query Match 89.4%; Score 59; DB 10; Length 30;
Best Local Similarity 92.9%; Pred. No. 8.3e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
|||||
Db 17 KTEISEVNLDAEF 30

RESULT 3
US-09-895-843-9
Sequence 9, Application US/09895843
Patent No. US20020143177A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gailunas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mailleard, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: TenBrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.41USU1
CURRENT APPLICATION NUMBER: US/09/895,843
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-895-843-9

Query Match 89.4%; Score 59; DB 10; Length 30;
Best Local Similarity 92.9%; Pred. No. 8.3e-05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
|||||
Db 17 KTEISEVNLDAEF 30

RESULT 4
US-09-896-874-4
Sequence 4, Application US/09896874
Patent No. US20020016320A1
GENERAL INFORMATION:
APPLICANT: Fang, Lawrence Y.
APPLICANT: John, Varghese
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.40USU1
CURRENT APPLICATION NUMBER: US/09/896,874
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-874-4

Query Match 89.4%; Score 59; DB 10; Length 32;
Best Local Similarity 92.9%; Pred. No. 8.9e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
|||||
Db 17 KTEISEVNLDAEF 30

RESULT 5
US-09-896-139-4
Sequence 4, Application US/09896139
Patent No. US20020128255A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gailunas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mailleard, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: TenBrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.25USU4
CURRENT APPLICATION NUMBER: US/09/896,139
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/268,497
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/279,779
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/295,589
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4

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; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-139-4

Query Match      89.4%; Score 59; DB 10; Length 32;
Best Local Similarity 92.9%; Pred. No. 8.9e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 17 KTEEISEVNLDAEF 30

RESULT 6
US-09-895-843-4
; Sequence 4, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailalaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-4

Query Match      89.4%; Score 59; DB 10; Length 32;
Best Local Similarity 92.9%; Pred. No. 8.9e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 17 KTEEISEVNLDAEF 30

RESULT 7
US-09-896-874-6
; Sequence 6, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-6

Query Match      89.4%; Score 59; DB 10; Length 33;
Best Local Similarity 92.9%; Pred. No. 9.3e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 20 KTEEISEVNLDAEF 33

RESULT 8
US-09-896-139-6
; Sequence 6, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailalaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-139-6

Query Match      89.4%; Score 59; DB 10; Length 33;
Best Local Similarity 92.9%; Pred. No. 9.3e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 20 KTEEISEVNLDAEF 33

RESULT 9
US-09-895-843-6
; Sequence 6, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
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us-09-724-571-97.rapb

Mon Nov 18 17:35:37 2002

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; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Vargnese
; APPLICANT: Mailaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-6

Query Match      89.4%; Score 59; DB 10; Length 33;
Best Local Similarity 92.9%; Pred. No. 9.3e-05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
    |||||
DB 20 KTEISEVNLDAEF 33

RESULT 10
US-09-794-927-12
; Sequence 12, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-12

Query Match      89.4%; Score 59; DB 10; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
    |||||
DB 587 KTEISEVNLDAEF 600

RESULT 12
US-09-794-743-12
; Sequence 12, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-12

Query Match      89.4%; Score 59; DB 10; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEISEVNLVAEF 14
    |||||
DB 587 KTEISEVNLDAEF 600

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; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-12

Query Match      89.4%; Score 59; DB 10; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 587 KTEEISEVNLDAEF 600

RESULT 13
US-09-794-748-12
; Sequence 12, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/62801L
; CURRENT APPLICATION NUMBER: US/09/794,748
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-12

Query Match      89.4%; Score 59; DB 10; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 587 KTEEISEVNLDAEF 600

RESULT 14
US-09-794-925-12
; Sequence 12, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/62801H
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
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; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-12

Query Match      89.4%; Score 59; DB 10; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

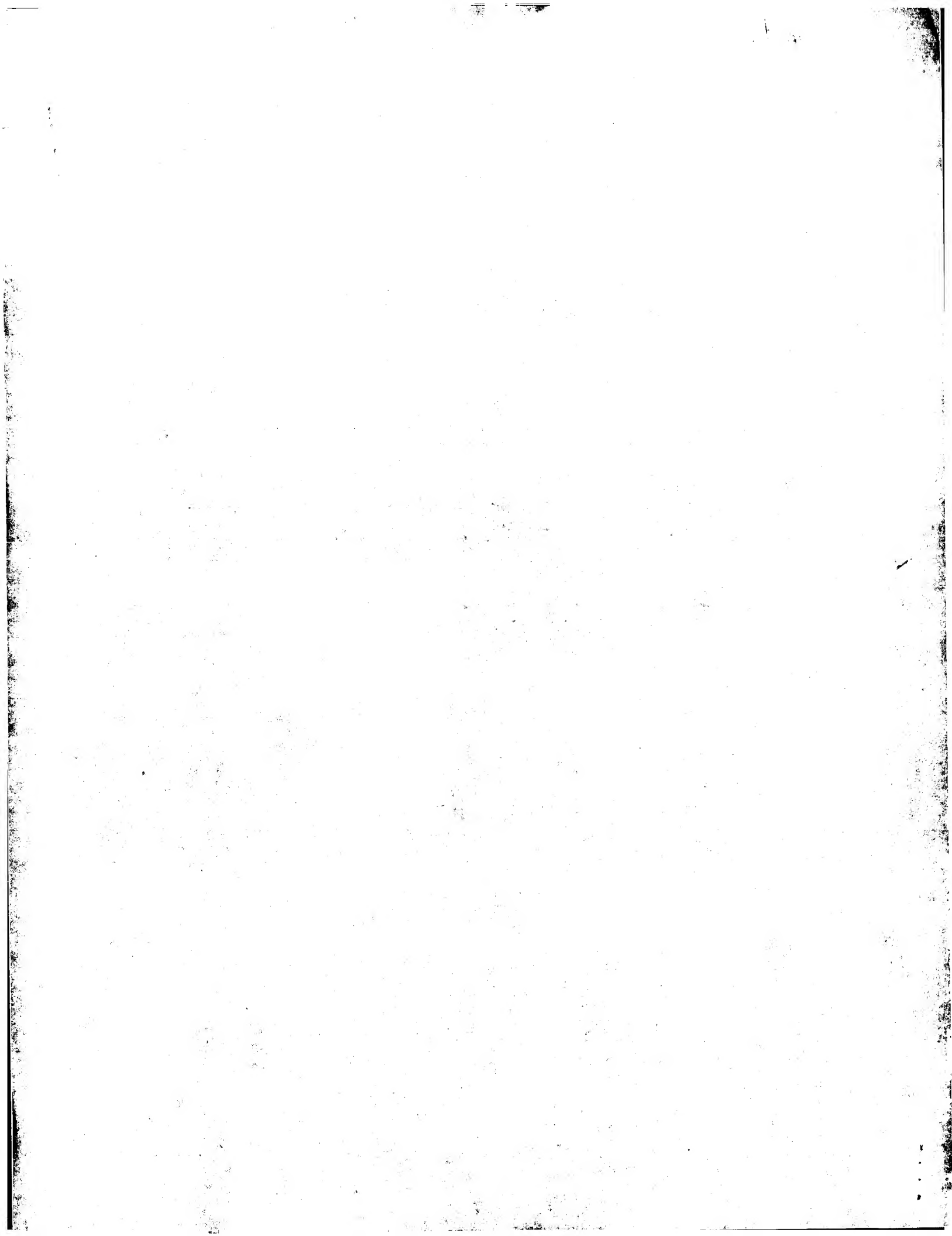
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Db 587 KTEEISEVNLDAEF 600

RESULT 15
US-09-681-442-12
; Sequence 12, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-12

Query Match      89.4%; Score 59; DB 10; Length 695;
Best Local Similarity 92.9%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTEEISEVNLVAEF 14
Db 587 KTEEISEVNLDAEF 600

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Job time : 8.52174 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:50:43 ; Search time 10.5652 Seconds
(without alignments)
81.892 Million cell updates/sec

Title: US-09-724-571-83
Perfect score: 44
Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	86.4	419	2 D42725	nitrite hydratase
2	38	86.4	4639	1 A54794	dynein heavy chain
3	36	81.8	33	2 S23094	beta-amyloid prote
4	36	81.8	57	2 E60045	Alzheimer's diseas
5	36	81.8	57	2 F60045	Alzheimer's diseas
6	36	81.8	57	2 G60045	Alzheimer's diseas
7	36	81.8	57	2 D60045	Alzheimer's diseas
8	36	81.8	57	2 A60045	Alzheimer's diseas
9	36	81.8	57	2 B60045	Alzheimer's diseas
10	36	81.8	82	2 PQ0438	Alzheimer's diseas
11	36	81.8	695	1 A49795	Alzheimer's diseas
12	36	81.8	695	2 A27485	Alzheimer's diseas
13	36	81.8	695	2 S00550	Alzheimer's diseas
14	36	81.8	770	1 QRHUA4	Alzheimer's diseas
15	35	79.5	265	2 S64127	Alzheimer's diseas
16	35	79.5	282	2 T26112	hypothetical prote
17	35	79.5	434	2 S72430	hypothetical prote
18	35	79.5	434	2 D88305	transcription elon
19	35	79.5	470	2 C75591	protein R03D7.4 [i
20	35	79.5	929	2 T52517	threonine synthase
21	35	79.5	1061	2 D98008	hypothetical prote
22	34	77.3	1024	2 C64208	hypothetical prote
23	33	75.0	442	2 B82633	nitrite hydratase
24	33	72.7	264	2 AG3466	transcription regu
25	32	72.7	287	2 AF0143	xanthosine phospho
26	32	72.7	345	2 E70162	DNA-directed RNA p
27	32	72.7	672	2 S52673	probable membrane
28	32	72.7	672	2 H86169	hypothetical prote
29	31	70.5	68	1 QOHSNB	hypothetical prote

30	31	70.5	68	2 B84267	hypothetical prote
31	31	70.5	233	2 T03329	probable amidase 1
32	31	70.5	253	2 S77778	probable NH(3)-dep
33	31	70.5	263	2 G72771	probable Prolifera
34	31	70.5	279	2 T41124	single-stranded DN
35	31	70.5	295	2 F83867	dihydrodipicolinat
36	31	70.5	324	2 A99435	hypothetical prote
37	31	70.5	351	2 S60963	hypothetical prote
38	31	70.5	368	2 A28825	keratin, type I no
39	31	70.5	395	2 F83873	hypothetical prote
40	31	70.5	397	2 B69760	conserved hypotHet
41	31	70.5	556	2 A99888	hypothetical prote
42	31	70.5	626	2 AF0358	conserved hypotHet
43	31	70.5	737	2 T31349	hypothetical prote
44	31	70.5	868	2 G82193	aminopeptidase N V
45	31	70.5	3351	2 T13812	lipophorin - fruit

ALIGNMENTS

RESULT 1
D42725

nitrite hydratase region 3'-hypothetical protein P47K - Pseudomonas chlororaphis (str
C:Species: Pseudomonas chlororaphis
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 20-Jun-2000
C:Accession: D42725
R:Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nagasawa, T.; Yamada, H.; Beppu, T.
J. Bacteriol. 173, 2465-2472, 1991
A:Title: Cloning and characterization of genes responsible for metabolism of nitrile
A:Reference number: A42725; MUID:91193202; PMID:2013568
A:Accession: D42725
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-419 <NLS>
A:Cross-references: GB:D90216; NID:g216850; PIDN:BAA14247.1; PID:g216854
C:Superfamily: conserved hypothetical protein yciC

Query Match 86.4%; Score 38; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SEVNLDAE 8
| | | | | | | |
Db 47 SEVNLDAE 54

RESULT 2

A54794
dynein heavy chain, cytosolic - fruit fly (Drosophila melanogaster)
N:Contains: dynein ATPase (EC 3.6.4.2)
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Apr-2002
C:Accession: A54794
R:Li, W.; McGrail, M.; Serr, M.; Hays, T.S.
J. Cell Biol. 126, 1475-1494, 1994
A:Title: Drosophila cytoplasmic dynein, a microtubule motor that is asymmetrically lo
A:Reference number: A54794; MUID:94375524; PMID:8089180
A:Accession: A54794
A:Molecule type: mRNA
A:Residues: 1-4639 <LIR>
A:Cross-references: GB:L23195; NID:g349668; PIDN:AAA60323.1; PID:g349669
C:Genetics:
A:Gene: FlyBase:Dhc64C
A:Cross-references: FlyBase:FBgn0010349
C:Superfamily: dynein heavy chain, cytosolic
C:Keywords: ATP; heterotetramer; hydrolase; microtubule binding; nucleotide binding;
F:1895-1902/Region: nucleotide-binding motif A (P-loop)
F:2210-2217/Region: nucleotide-binding motif A (P-loop)
F:2580-2587/Region: nucleotide-binding motif A (P-loop)
F:2922-2929/Region: nucleotide-binding motif A (P-loop)
F:1901/Binding site: ATP (Lys) #status predicted
F:2216/Binding site: ATP (Lys) #status predicted

F;2586/Binding site: ATP (Lys) #status predicted
F;2928/Binding site: ATP (Lys) #status predicted

Query Match 86.4%; Score 38; DB 1; Length 4639;
Best Local Similarity 88.9%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
||| :|||||
Db 3882 SESNLDADF 3890

RESULT 3
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198; PMID:1618299
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <KQJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 81.8%; Score 36; DB 2; Length 33;
Best Local Similarity 77.8%; Pred. No. 0.47;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
||| :||||
Db 1 SEVKMDADF 9

RESULT 4
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 81.8%; Score 36; DB 2; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
||| :||||
Db 1 SEVKMDADF 9

RESULT 5
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045

A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; PIDN:CAA39592.1; PID:q1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 81.8%; Score 36; DB 2; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
||| :||||
Db 1 SEVKMDADF 9

RESULT 6
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 81.8%; Score 36; DB 2; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
||| :||||
Db 1 SEVKMDADF 9

RESULT 7
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 81.8%; Score 36; DB 2; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
||| :||||
Db 1 SEVKMDADF 9

RESULT 8
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 81.8%; Score 36; DB 2; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
||| :||||
DB 1 SEVKMDAEF 9

RESULT 9
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 81.8%; Score 36; DB 2; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
||| :||||
DB 1 SEVKMDAEF 9

RESULT 10
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: PQ0438; MUID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83658; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 81.8%; Score 36; DB 2; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
||| :||||
DB 12 SEVKMDAEF 20

RESULT 11
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 81.8%; Score 36; DB 1; Length 695;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
||| :||||
DB 592 SEVKMDAEF 600

RESULT 12
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuwa, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 81.8%; Score 36; DB 2; Length 695;

A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:9236720; PIDN:AAB19991.1; PID:g236721
R:Kamino, K.; Ori, H.T.; Payami, H.; Wajsmann, E.M.; Alonso, M.E.; Pulist, S.M.; Anderson, arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukulski, W.; Larson, E.; Heston, L.L.; Martin, Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the A:Reference number: A44017; MUID:9305397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAMI>
A:Cross-references: GB:SA5135; NID:9257377; PIDN:AAB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:SA5136; NID:9257379; PIDN:AAB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M. Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C. Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:9178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)

R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H. Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasooli, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, Query Match 81.8%; Score 36; DB 1; Length 770;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SEVNLDAEF 9
| | | | |
Db 667 SEVKMDAEF 675
RESULT 15
S64127
hypothetical protein YGL17w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G2935
C:Species: Saccharomyces cerevisiae
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C:Accession: S64127
R:Laquin, G.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64122
A:Accession: S64127
A:Molecule type: DNA
A:Residues: 1-265 <LAU>
A:Cross-references: EMBL:Z72639; NID:91322670; PID:e243345; PID:g1322671; GSPDB:GN000
A:Experimental source: strain S288C
C:Genetics:

Mon Nov 18 17:35:35 2002

A;Gene: MIPS:YGL117w
A;Cross-references: SGD:S0003085
A;Map position: 7L

Query Match 79.5%; Score 35; DB 2; Length 265;
Best Local Similarity 77.8%; Pred. No. 8.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDNEF 9
|:|||||
DB 238 SDVNLDNEF 246

Search completed: November 18, 2002, 12:54:06
Job time : 12.5652 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:49:38 ; Search time 5.86957 Seconds
(without alignments)
53.597 Million cell updates/sec

Title: US-09-724-571-83
Perfect score: 44
Sequence: 1 SEVNLDADF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	38	86.4	419	1 P47K_PSECL	P31521 pseudomonas
2	38	86.4	4639	1 DYHC_DROME	P37276 drosophila
3	36	81.8	57	1 A4_PIG	Q29023 sus scrofa
4	36	81.8	57	1 A4_URMA	Q29149 ursus marit
5	36	81.8	58	1 A4_CANFA	Q28280 canis famil
6	36	81.8	58	1 A4_RABIT	Q28748 oryctolagus
7	36	81.8	58	1 A4_SHEEP	Q28757 ovis aries
8	36	81.8	59	1 A4_BOVIN	Q28053 bos taurus
9	36	81.8	751	1 A4_SATSC	Q95241 saimiri sci
10	36	81.8	770	1 A4_HUMAN	P05067 homo sapien
11	36	81.8	770	1 A4_MOUSE	P12023 mus musculu
12	36	81.8	770	1 A4_RAT	P08592 rattus norv
13	35	79.5	265	1 YGL7_YEAST	P53133 saccharomyc
14	35	79.5	434	1 YRL4_CAEEL	Q09413 caenorhabdi
15	34	77.3	1024	1 Y075_MYCGE	P47321 mycoplasma
16	32	72.7	345	1 RPOA_BORBU	O51455 borrelia bu
17	32	72.7	383	1 ALR_BACPS	Q955v6 bacillus ps
18	31	70.5	68	1 YB10_HALN1	P17104 halobacteri
19	31	70.5	279	1 RFA2_SCHPO	Q92373 schizosacch
20	31	70.5	295	1 DAP1_BACHD	Q9Kc32 bacillus ha
21	31	70.5	312	1 IF2B_DROME	P41375 drosophila
22	31	70.5	351	1 YN04_YEAST	P53892 saccharomyc
23	31	70.5	368	1 K1CR_XENLA	P08802 xenopus lae
24	31	70.5	3562	1 PGCV_CHICK	Q09053 gallus gall
25	30	68.2	126	1 PFD4_CAEEL	Q17435 caenorhabdi
26	30	68.2	303	1 LMB1_CHICK	Q01635 gallus gall
27	30	68.2	326	1 V72_MTXVL	P29825 myxoma viru
28	30	68.2	345	1 CC14_CAEEL	P18834 caenorhabdi
29	30	68.2	404	1 HIS2_ANASP	Q8Yt12 anabaena sp
30	30	68.2	426	1 RAD9_SCHPO	P26306 schizosacch
31	30	68.2	433	1 MTH1_YEAST	P35198 saccharomyc
32	30	68.2	497	1 GLYA_CHLMU	Q9Pjw0 chlamydia m
33	30	68.2	497	1 GLYA_CHLTR	O84439 chlamydia t

34 30 68.2 1462 1 PTP6_DROME P16620 drosophila
35 29 65.9 232 1 YC10_PSEAE Q914c8 pseudomonas
36 29 65.9 246 1 CAH_KLEPN O52535 klebsiella
37 29 65.9 272 1 T2F1_HAEIN P20588 haemophilus
38 29 65.9 289 1 YERO_BACSU O31500 bacillus su
39 29 65.9 340 1 RPOA_STRCO P72104 streptomyce
40 29 65.9 340 1 RPOA_STRGT Q9x4v6 streptomyce
41 29 65.9 350 1 RPOS_SHIFL O32874 shigella fl
42 29 65.9 382 1 METX_MYCLE O32874 mycobacteri
43 29 65.9 394 1 ALR2_BACSU P94425 ciona intes
44 29 65.9 413 1 SYI_CIOIN Q94425 ciona intes
45 29 65.9 469 1 RECI_METJA Q58387 methanococc

ALIGNMENTS

RESULT 1
P47K_PSECL
ID P47K_PSECL STANDARD; PRT: 419 AA.
AC P31521;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 47 kDa protein (P47K).
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
RX NCBI_TaxID=333;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B23;
RX MEDLINE=911933202; PubMed=2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
Beppu T.;
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23.";
RL J. Bacteriol. 173:2465-2472(1991).
CC -!- FUNCTION: THE PRESENCE OF P47K IS CRITICAL FOR THE EXPRESSION
CC OF THE NITRILE HYDRATASE GENES. MAY STABILIZE OR ACTIVATE THE
CC NITRILE HYDRATASE PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; D90216; BAA14247.1; -
CC FIR; D42725; D42725.
CC InterPro; IPR003495; Codbw.
CC Pfam; PF02492; codbw; 1.
SQ SEQUENCE 419 AA: 46566 MW; FF5113800E27FF0C CRC64;
Query Match 86.4%; Score 38; DB 1; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLDAA 8
Db 47 SEVNLDAA 54
RESULT 2
DYHC_DROME
ID DYHC_DROME STANDARD; PRT: 4639 AA.
AC P37276;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).

```
GN CDHC OR DHC64C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94375524; PubMed=8089180;
RA Li M., McGrail M., Serr M., Hays T.S.;
RT "Drosophila cytoplasmic dynein, a microtubule motor that is
RT asymmetrically localized in the oocyte.";
RL J. Cell Biol. 126:1475-1494(1994).
RN [2]
RP SEQUENCE OF 1877-1998 FROM N.A.
RX MEDLINE=94243034; PubMed=8186464;
RA Rasmussen K., Serr M., Gerner J., Gibbons I., Hays T.S.;
RT "A family of dynein genes in Drosophila melanogaster.";
RL Mol. Biol. Cell 5:45-55(1994).
CC -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A
CC MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
CC ORGANELLES ALONG MICROTUBULES.
CC -!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
CC INTERMEDIATE AND LIGHT CHAINS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L23195; AAA60323.1; -.
DR EMBL; L25122; AAA28492.1; -.
DR FlyBase; FBgn0010349; Dhc64C.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
FT DOMAIN 530 565
FT COILED COIL (POTENTIAL).
FT DOMAIN 774 794
FT COILED COIL (POTENTIAL).
FT DOMAIN 1264 1368
FT COILED COIL (POTENTIAL).
FT DOMAIN 1999 2027
FT MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 3189 3261
FT COILED COIL (POTENTIAL).
FT DOMAIN 3382 3478
FT COILED COIL (POTENTIAL).
FT DOMAIN 3723 3782
FT COILED COIL (POTENTIAL).
FT NP_BIND 1895 1902
FT ATP (POTENTIAL).
FT NP_BIND 2210 2217
FT ATP (POTENTIAL).
FT NP_BIND 2580 2587
FT ATP (POTENTIAL).
FT NP_BIND 2922 2929
FT ATP (POTENTIAL).
SQ SEQUENCE 4639 AA; 530152 MW; 057A7D8800CCD07E CRC64;

Query Match 86.4%; Score 38; DB 1; Length 4639;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
DB 3882 SEVNLDAEF 3890

RESULT 3
A4_PIG
ID A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
```

```
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56127; CAA39592.1; -.
DR HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF03494; Beta_APP; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48
FT DOMAIN <1 33
FT TRANSMEM 34 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 81.8%; Score 36; DB 1; Length 57;
Best Local Similarity 77.8%; Pred. No. 0.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
DB 1 SEVKMDAEF 9

RESULT 4
A4_URMSA
ID A4_URMSA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RN [2]
RP SEQUENCE OF 1877-1998 FROM N.A.
RX MEDLINE=94243034; PubMed=8186464;
RA Rasmussen K., Serr M., Gerner J., Gibbons I., Hays T.S.;
RT "A family of dynein genes in Drosophila melanogaster.";
RL Mol. Biol. Cell 5:45-55(1994).
CC -!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A
CC MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND
CC ORGANELLES ALONG MICROTUBULES.
CC -!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
CC INTERMEDIATE AND LIGHT CHAINS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
CC -----
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CC -----
DR EMBL; L23195; AAA60323.1; -.
DR EMBL; L25122; AAA28492.1; -.
DR FlyBase; FBgn0010349; Dhc64C.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
KW Motor protein; Microtubules; Dynein; ATP-binding; Coiled coil.
FT DOMAIN 530 565
FT COILED COIL (POTENTIAL).
FT DOMAIN 774 794
FT COILED COIL (POTENTIAL).
FT DOMAIN 1264 1368
FT COILED COIL (POTENTIAL).
FT DOMAIN 1999 2027
FT MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 3189 3261
FT COILED COIL (POTENTIAL).
FT DOMAIN 3382 3478
FT COILED COIL (POTENTIAL).
FT DOMAIN 3723 3782
FT COILED COIL (POTENTIAL).
FT NP_BIND 1895 1902
FT ATP (POTENTIAL).
FT NP_BIND 2210 2217
FT ATP (POTENTIAL).
FT NP_BIND 2580 2587
FT ATP (POTENTIAL).
FT NP_BIND 2922 2929
FT ATP (POTENTIAL).
SQ SEQUENCE 4639 AA; 530152 MW; 057A7D8800CCD07E CRC64;

Query Match 86.4%; Score 38; DB 1; Length 4639;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
DB 3882 SEVNLDAEF 3890

RESULT 3
A4_PIG
ID A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
```



```
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CAA39593.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC Pfam; PF03494; Beta-APP; 1.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57
CC NON_TER 57 57
CC SEQUENCE 57 AA; 6172 MW; 84209D88EA82DFA CRC64;
CC -----
CC Query Match 81.8%; Score 36; DB 1; Length 57;
CC Best Local Similarity 77.8%; Pred. No. 0.4;
CC Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 1 SEVNLDAEF 9
DB 1 SEVKMDAEF 9
III : IIII
1 SEVKMDAEF 9
-----
RESULT 5
A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56125; CAA39590.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC Pfam; PF03494; Beta-APP; 1.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 7 49 BETA-AMYLLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 35 58
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
CC -----
CC Query Match 81.8%; Score 36; DB 1; Length 58;
CC Best Local Similarity 77.8%; Pred. No. 0.41;
CC Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 1 SEVNLDAEF 9
DB 2 SEVKMDAEF 10
III : IIII
2 SEVKMDAEF 10
-----
RESULT 6
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56129; CAA39594.1; -.
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC Pfam; PF03494; Beta-APP; 1.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
```

QY	1 SEVNLDAEF 9						
	:						
DB	1 SEVKMDAEF 9						
RESULT 8							
A4_BOVIN	STANDARD;	PRT;	59 AA.				
ID	A4_BOVIN						
AC	Q28053;						
DT	01-NOV-1997 (Rel. 35, Created)						
DT	01-NOV-1997 (Rel. 35, Last sequence update)						
DT	30-MAY-2000 (Rel. 39, Last annotation update)						
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid						
DE	protein (Beta-APP) (A-beta)] (Fragment).						
GN	APP.						
OS	Bos taurus (Bovine).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;						
OC	Bovidae; Bovinae; Bos.						
OX	NCBI_TaxID=9913;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Brain;						
RX	MEDLINE=92017079; PubMed=1656157;						
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;						
RT	"Conservation of the sequence of the Alzheimer's disease amyloid						
RT	peptide in dog, polar bear and five other mammals by cross-species						
RT	polymerase chain reaction analysis.";						
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).						
CC	!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO						
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN						
CC	G(O) (BY SIMILARITY).						
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.						
CC	!- SIMILARITY: BELONGS TO THE APP FAMILY.						
CC	-----						
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CC	or send an email to license@isb-sib.ch).						
CC	-----						
DR	EMBL; X56124; CAA39589.1; -.						
DR	EMBL; X56126; CAA39591.1; -.						
DR	HSP; P05067; 1BA4.						
DR	InterPro; IPR001868; A4_APP.						
DR	InterPro; IPR001255; Beta-APP.						
DR	Pfam; PF03494; Beta-APP; 1.						
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.						
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.						
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.						
FT	NON_TER	1					
FT	CHAIN	1	49	BETA-AMYLOID PROTEIN (POTENTIAL).			
FT	DOMAIN	<1	34	EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM	35	58	POTENTIAL.			
FT	DOMAIN	59	>59	CYTOPLASMIC (POTENTIAL).			
FT	NON_TER	59	59				
SQ	SEQUENCE	59 AA;	6414 MW;	F43469D488A2E12D CRC64;			
Query Match							
Best Local Similarity		81.8%;		Score 36; DB 1; Length 59;			
Matches		7; Conservative		1; Mismatches 1; Indels 0; Gaps 0;			
QY	1 SEVNLDAEF 9						
	:						
DB	2 SEVKMDAEF 10						
RESULT 9							
A4_SAISC	STANDARD;	PRT;	751 AA.				
ID	A4_SAISC						

Q95241;
 15-DEC-1998 (Rel. 37, Created)
 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
 amyloid protein (Beta-APP) (A-beta)].
 GN APP
 OS Saimiri sciureus (Common squirrel monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 cerebral amyloid angiopathy".
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC -----
 DR EMBL: S81024; AADI4347.1; -;
 DR HSP; P05067; IAA.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 KW Signal; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 553 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 81.8%; Score 36; DB 1; Length 751;
 Best Local Similarity 77.8%; Pred. No. 6.8;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SEYNLDAEF 9
 DB 648 SEVKMDAEF 656
 III :IIII
 RESULT 10
 A4_HUMAN
 ID A4_HUMAN STANDARD; PRT; 770 AA.
 AC P05067; P09000; Q16011;
 DT 13-NOV-1987 (Rel. 05, Created)
 DT 01-AUG-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
 DE (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP OR A4 OR CVAP OR AD1.
 OS Homo sapiens (human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor".
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors".
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons".
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhashi H., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus".
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease".
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity".
 RL Nature 331:530-532(1988).

RN SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RP MEDLINE=87231971; PubMed=3035574;
 RX Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RA "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 [7]
 RN SEQUENCE OF 507-770 FROM N.A.
 RP MEDLINE=88124954; PubMed=2893379;
 RX Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RA "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RL mRNA are expressed in the cortex.";
 [9]
 RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 [8]
 RN SEQUENCE OF 672-681.
 RP MEDLINE=88035004; PubMed=3312495;
 RX Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RA "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RL microvessels.";
 [10]
 RN J. Neurochem. 49:1394-1401(1987).
 [11]
 RN SEQUENCE OF 1-10 FROM N.A.
 RP MEDLINE=90236318; PubMed=2110105;
 RX Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RA "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 [12]
 RN Gene 87:257-263(1990).
 [13]
 RN TISSUE=Liver;
 RP MEDLINE=89016647; PubMed=3140222;
 RX Schon E.A., Mita S., Sadlock J., Herbert J.;
 RA "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 [14]
 RN Nucleic Acids Res. 16:9351-9351(1988).
 [15]
 RN SEQUENCE OF 18-50.
 RP MEDLINE=87250462; PubMed=3597385;
 RX van Nostrand W.E., Cunningham D.D.;
 RA "Purification of protease nexin II from human fibroblasts.";
 [16]
 RN J. Biol. Chem. 262:8508-8514(1987).
 [17]
 RN IDENTITY OF APP WITH NEXIN-II.
 RP MEDLINE=89384866; PubMed=2506449;
 RX Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RA "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 [18]
 RN Nature 341:144-147(1989).
 [19]
 RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RP MEDLINE=90211252; PubMed=1969731;
 RX Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RA "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 [20]
 RN Biochem. Biophys. Res. Commun. 167:716-721(1990).
 [21]
 RN COMPLEX WITH G(O).
 RP MEDLINE=93188965; PubMed=8446172;
 RX Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RA "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 [22]
 RN Nature 362:75-79(1993).
 [23]
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RP MEDLINE=99215582; PubMed=10201399;

RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RA "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 [17]
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RP MEDLINE=91104913; PubMed=2125487;
 RX Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
 RA "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 [18]
 RN STRUCTURE BY NMR OF 289-344.
 RP MEDLINE=92031488; PubMed=1718421;
 RX Heald S.D., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RA "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RL precursor protein.";
 [19]
 RN Biochemistry 30:10467-10478(1991).
 [20]
 RN STRUCTURE BY NMR OF 672-699.
 RP MEDLINE=94281210; PubMed=7516706;
 RX Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;
 RA "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 [21]
 RN STRUCTURE BY NMR OF 696-706.
 RP MEDLINE=97128622; PubMed=8973180;
 RX Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RA "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 [22]
 RN STRUCTURE BY NMR OF 672-711.
 RP MEDLINE=98359783; PubMed=9693002;
 RX Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RA "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 [23]
 RN STRUCTURE BY NMR OF 672-699.
 RP MEDLINE=20400066; PubMed=10940222;
 RX Poulsen S.-A., Watson A.A., Craik D.J.;
 RA "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RL site.";
 [24]
 RN J. Struct. Biol. 130:142-152(2000).
 [25]
 RN STRUCTURE BY NMR OF 681-706.
 RP MEDLINE=20400065; PubMed=10940221;
 RX Zhang S., Iwata K., Lachmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RA "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 [26]
 RN J. Struct. Biol. 130:130-141(2000).
 [27]
 RN SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RP MEDLINE=88296437; PubMed=2900137;
 RX Dyrks J., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RA "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";

Query Match 81.8%; Score 36; Length 770;
 Best Local Similarity 77.8%; Pred. No. 6.9;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SEYNLDAEF 9
 ||| :|||

Db 667 SEVKMDAEF 675

RESULT 11

A4_MOUSE

ID A4_MOUSE STANDARD; PRT; 770 AA.

AC P12023;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor

DE (Amyloidogenic glycoprotein) (AG).

GN App.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC STRAIN=BAIB/C; TISSUE=Brain;

RX MEDLINE=92096458; PubMed=1756177;

RA de Strooper B., van Leuven F., van den Berghe H.;

RT "The amyloid beta protein precursor or proteinase nexin II from mouse

RT is closer related to its human homolog than previously reported.";

RL Biochim. Biophys. Acta 1129:141-143(1991).

RN [2]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=88106489; PubMed=3322280;

RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;

RT "Complementary DNA for the mouse homolog of the human amyloid beta

RT protein precursor.";

RL Biochem. Biophys. Res. Commun. 149:665-671(1987).

RN [3]

RP REVISIONS.

RA Yamada T.;

RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 289-364 FROM N.A.

RC STRAIN=CD-1; TISSUE=Placenta;

RX MEDLINE=89145111; PubMed=2569710;

RA Fukuchi K., Martin G.M., Deeb S.S.;

RT "Sequence of the protease inhibitor domain of the A4 amyloid protein

RT precursor of Mus domesticus.";

RL Nucleic Acids Res. 17:5396-5396(1989).

RN [5]

RP SEQUENCE OF 1-19 FROM N.A.

RX MEDLINE=92209998; PubMed=1555768;

RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,

RA Sakai Y.;

RT "Positive and negative regulatory elements for the expression of the

RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";

RL Gene 112:189-195(1992).

RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=Brain, and Kidney;

RX MEDLINE=89149813; PubMed=2493250;

RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;

RT "Structure and expression of the alternatively-spliced forms of mRNA

RT for the mouse homolog of Alzheimer's disease amyloid beta protein

RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).

CC -|- SUBCELLULAR LOCATION: Type I membrane protein.

CC -|- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),

CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE

CC SPLICING.

CC -|- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS

CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND

CC LIVER.

CC -|- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION

CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC

CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE

CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF

CC

CC PHOSPHORYLATION (BY SIMILARITY).

CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -|- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

CC

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CC -----

CC EMBL; X59379; ; NOT_ANNOTATED_CDS.

CC EMBL; M18373; AAA37139.1; -

CC EMBL; X15210; CAA33280.1; -

CC EMBL; D10603; BAA01456.1; -

CC EMBL; M24397; AAA39929.1; -

CC PIR; A27485; A27485.

CC PIR; S04855; S04855.

CC PIR; S19727; S19727.

CC HSP; P05067; IAAI.

CC MGI; MGI:88059; App.

CC InterPro; IPR001868; A4_APP.

CC InterPro; IPR001255; Beta-APP.

CC InterPro; IPR002223; Kunitz_BPTI.

CC Pfam; PF00114; Kunitz_BPTI; 1.

CC Pfam; PF02177; A4_EXTRA; 1.

CC Pfam; PF03494; Beta-APP; 1.

CC PRINTS; PR00203; AMYLOIDA4.

CC PRINTS; PR00759; BASICPTASE.

CC ProDom; PD000222; Kunitz_BPTI; 1.

CC SMART; SM00006; A4_EXTRA; 1.

CC SMART; SM00131; KO; 1.

CC PROSITE; PS00319; A4_EXTRA; 1.

CC PROSITE; PS00320; A4_INTRA; 1.

CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.

CC Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

CC Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17

FT CHAIN 18 770

FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT HOMOLOG.

FT DOMAIN 18 699

FT TRANSMEM 700 723

FT POTENTIAL.

FT DOMAIN 724 770

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 673 715

FT EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT DOMAIN 287 345

FT BPTI/KUNITZ INHIBITOR.

FT SITE 759 762

FT CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 291 341

FT BY SIMILARITY.

FT DISULFID 300 324

FT BY SIMILARITY.

FT DISULFID 316 337

FT BY SIMILARITY.

FT CARBOHYD 542 542

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 571 571

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPPLIC 289 289

FT E -> V (IN ISOFORM APP(695)).

FT VARSPPLIC 290 364

FT MISSING (IN ISOFORM APP(695)).

FT VARSPPLIC 346 380

FT MISSING (IN ISOFORM APP(751)).

SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;

Query Match 81.8%; Score 36; DB 1; Length 770;

Best Local Similarity 77.8%; Pred. No. 6.9;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SEVNLDAEF 9

Db 667 SEVKMDAEF 675

RESULT 12

A4_RAT

ID A4_RAT STANDARD; PRT; 770 AA.

AC P08592;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT

16-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein homolog precursor
(Amyloidogenic glycoprotein) (AG).
APP.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE OF 1-289 AND 365-770 FROM N.A.
TISSUE=Brain;
MEDLINE=88312593; PubMed=2900758;
Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
Seeburg P.H.; disease amyloidogenic glycoprotein: expression pattern
in rat brain suggests a role in cell contact.;
EMBO J. 7:1365-1370(1988).
[2]
SEQUENCE OF 289-364 FROM N.A.
TISSUE=Liver;
MEDLINE=89183625; PubMed=2648331;
Kang J., Mueller-Hill B.;
"The sequence of the two extra exons in rat preA4.";
Nucleic Acids Res. 17:2130-2130(1989).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
SPlicing.
CC -! DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
PHOSPHORYLATION (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE APP FAMILY.
CC -! SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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EMBL; X07648; CAA30488.1; .
EMBL; X14066; CAA32229.1; .
DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSP; P05067; 1AAP.
DR InterPro; IPRO01868; A4_APP.
DR InterPro; IPRO01255; Beta_APP.
DR InterPro; IPRO02223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPFASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR ProDom; PD000006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR GlycoProtex; Amyloid; Neutrone; Transmembrane; Signal;
KW Glycopolymers; Amyloid; Neutrone; Protease inhibitor.
Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT HOMOLOG.
FT DOMAIN 18 699
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 724 770
FT CATABOLISM OF BETA-AMYLOID PROTEIN.

FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT BY SIMILARITY.
FT DISULFID 300 324
FT BY SIMILARITY.
FT DISULFID 316 337
FT BY SIMILARITY.
FT CARBOHYD 542 542
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 571 571
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPPLIC 289 289
FT MISSING (IN ISOFORM APP(695)).
FT VARSPLIC 290 364
FT SEQUENCE 770 AA; 86704 MW; C26C9D8BB2D929A7 CRC64;
SQ
Query Match 81.8%; Score 36; DB 1; Length 770;
Best Local Similarity 77.8%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SEVNLDAEF 9
DB 667 SEVKMDAEF 675
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RESULT 13
YGL7_YEAST STANDARD; PRT; 265 AA.
ID YGL7_YEAST
AC P53133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 30.8 kDa protein in ABC1-CDC20 intergenic region.
GN YGL117W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Lauquin G.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
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EMBL; Z72639; CAA96825.1; .
DR SGD; S0003085; YGL117W.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 30755 MW; 7BB5E25246CEB75F CRC64;
Query Match 79.5%; Score 35; DB 1; Length 265;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 SEVNLDAEF 9
DB 238 SDVNLDNEF 246
|||||
RESULT 14
YRL4_CAEL STANDARD; PRT; 434 AA.
ID YRL4_CAEL
AC Q09413;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 49.2 kDa protein R03D7.4 in chromosome II.
GN R03D7.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

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RN
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Swinburne J.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; Z46828; CAA86857.1; -
DR Wormpep; R03D7.4; CE01611.
KW Hypothetical protein.
FT DOMAIN 154 159 POLY-SER.
FT DOMAIN 407 414 POLY-ASN.
SQ SEQUENCE 434 AA; 49240 MW; EB0A02A996ED0844 CRC64;

Query Match          79.5%; Score 35; DB 1; Length 434;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVNLDAEF 9
Db 97 EVNLDDEF 104

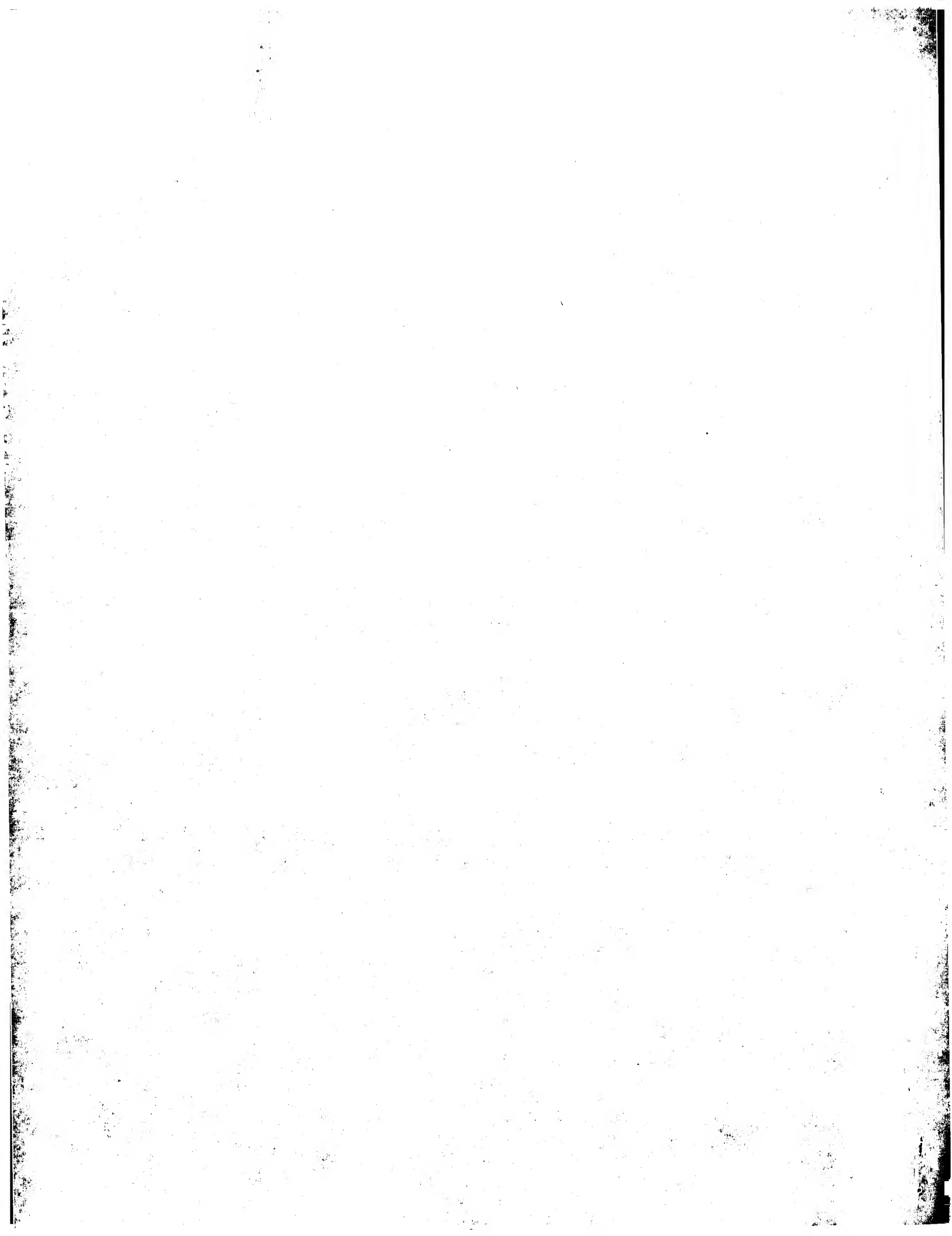
RESULT 15
Y075_MYCGE
ID Y075_MYCGE STANDARD; PRT; 1024 AA.
AC R47321; Q49190;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG075.
GN MG075.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 1-156; 269-402; 643-736 AND 808-947 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL; U39688; AAC71293.1; -
DR EMBL; U01715; AAC43189.1; ALT_INIT.
```

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DR EMBL; U02251; AAD12514.1; -
DR EMBL; U01749; AAD10562.1; -
DR EMBL; U01775; AAD10595.1; -
DR TIGR; MG075; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 951 971 POTENTIAL.
SQ SEQUENCE 1024 AA; 116424 MW; 5B1540E6855CB554 CRC64;

Query Match          77.3%; Score 34; DB 1; Length 1024;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
Db 150 SEVSLDLEF 158

Search completed: November 18, 2002, 12:52:35
Job time : 6.86957 secs
```



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:50:24 : Search time 19,1739 Seconds
(without alignments)
96.716 Million cell updates/sec

Title: US-09-724-571-83
Perfect score: 44
Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	86.4	779	5 Q9w1b1	Q9w1b1 drosophila
2	38	86.4	839	5 Q961m8	Q961m8 drosophila
3	38	86.4	4623	5 Q9vz83	Q9vz83 drosophila
4	36	81.8	35	4 Q8wz99	Q8wz99 homo sapien
5	36	81.8	79	11 Q35463	Q35463 cricetus
6	36	81.8	82	4 Q16014	Q16014 homo sapien
7	36	81.8	82	4 Q16019	Q16019 homo sapien
8	36	81.8	82	4 Q16020	Q16020 homo sapien
9	36	81.8	82	4 P78438	P78438 homo sapien
10	36	81.8	534	13 Q93296	Q93296 gallus gall
11	36	81.8	569	13 Q9pvl1	Q9pvl1 gallus gall
12	36	81.8	607	11 Q99k32	Q99k32 mus musculus
13	36	81.8	695	6 Q95kn7	Q95kn7 macaca fasc
14	36	81.8	695	11 Q60496	Q60496 cavia sp. p
15	36	81.8	695	11 P97487	P97487 mus musculus
16	36	81.8	695	13 Q9dgs8	Q9dgs8 gallus gall

17	36	81.8	751	13	Q9dgsj7	Q9dgsj7 gallus gall
18	36	81.8	770	6	Q9tui0	Q9tui0 sus scrofa
19	35	79.5	282	5	O02335	O02335 caenorhabditis
20	35	79.5	470	16	Q9ryf8	Q9ryf8 deinoecoccus
21	35	79.5	859	3	Q9hfi9	Q9hfi9 neurospora
22	35	75.0	143	4	Q9h935	Q9h935 homo sapien
23	33	75.0	294	17	Q96xw4	Q96xw4 sulfolobus
24	33	75.0	405	4	Q98u21	Q98u21 homo sapien
25	33	75.0	442	16	Q9pcf1	Q9pcf1 xylella fas
26	33	75.0	460	17	Q8zt64	Q8zt64 pyrobaculum
27	33	75.0	539	4	Q9nwd6	Q9nwd6 homo sapien
28	33	75.0	539	4	Q9nw45	Q9nw45 homo sapien
29	33	75.0	602	5	Q95rl2	Q95rl2 drosophila
30	33	75.0	614	4	Q8wu94	Q8wu94 homo sapien
31	33	75.0	614	4	Q96sr8	Q96sr8 homo sapien
32	33	75.0	1181	5	Q9v795	Q9v795 drosophila
33	32.5	73.9	557	13	Q90z52	Q90z52 brachydanio
34	32	72.7	178	2	Q93te3	Q93te3 pseudomonas
35	32	72.7	264	16	Q8yfi10	Q8yfi10 brucella me
36	32	72.7	287	16	Q8zgv4	Q8zgv4 yersinia pe
37	32	72.7	289	10	Q9auv5	Q9auv5 oryza sativ
38	32	72.7	308	10	Q8s7m4	Q8s7m4 oryza sativ
39	32	72.7	357	10	Q8s7m2	Q8s7m2 oryza sativ
40	32	72.7	608	17	Q8ztj3	Q8ztj3 pyrobaculum
41	32	72.7	672	3	Q04562	Q04562 saccharomyc
42	32	72.7	672	10	Q92wb1	Q92wb1 arabidopsis
43	32	72.7	867	9	Q9zx10	Q9zx10 mycobacteri
44	32	72.7	1250	2	Q93n06	Q93n06 campylobact
45	31	70.5	84	17	Q8tiw2	Q8tiw2 methanosarc

ALIGNMENTS

RESULT 1

Q9w1b1	PRELIMINARY:	PRT:	779 AA.
AC	Q9w1b1		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	CG16786 protein.		
OS	CG16786		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY;		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-pfannkuch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarri C., Morris J., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nixon K., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003463; AAF47161.1;
DR FlyBase: FBgn0034974; CG16786.
SQ SEQUENCE 779 AA; 86335 MW; E1231D45CB01A15E CRC64;

Query Match 86.4%; Score 38; DB 5; Length 779;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
Db 570 SEINLDLEF 578

RESULT 2
Q961M8 PRELIMINARY; PRT; 839 AA.
ID Q961M8
AC Q961M8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE GH15453p.
GN DHC64C OR CG7507.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN STRAIN=BERKELEY;
RC Palazzolo M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY051501; AK92925.1;
DR FlyBase: FBgn0010349; Dhc64C.
DR InterPro: IPR004273; Dynein_heavy.
DR Pfam: PF03028; Dynein_heavy; 1.
SQ SEQUENCE 839 AA; 94472 MW; 038B81350D706C0C CRC64;

Query Match 86.4%; Score 38; DB 5; Length 839;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
Db 82 SESNLDAEF 90

RESULT 3
Q9VZ83 PRELIMINARY; PRT; 4623 AA.
ID Q9VZ83
AC Q9VZ83
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DHC64C protein.
GN DHC64C OR CG7507.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulo G., Milshina N.V., Mobarri C., Morris J., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RL "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003462; AAF47942.2;
DR FlyBase: FBgn0010349; Dhc64C.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR004273; Dynein_heavy.
DR InterPro: IPR000169; SHprot_acsite.
DR Pfam: PF03028; Dynein_heavy; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00639; THIOLEPROTEASE_HIS; UNKNOWN_1.
SQ SEQUENCE 4623 AA; 528403 MW; 0E03827AA75818D0 CRC64;

Query Match 86.4%; Score 38; DB 5; Length 4623;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
Db 3866 SESNLDAEF 3874

RESULT 4
Q8WZ99 PRELIMINARY; PRT; 35 AA.
ID Q8WZ99

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AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DE Beta-amyloid peptide (Fragment).
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DE Amyloid protein (Fragment).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wakutani Y., Nimomiya H., Iwata H., Tanaka S., Urakami K., Adachi Y.,
RA Wada-Isoe K., Yamagata K., Ohono K., Tsubuki S., Saido T.,
RA Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel missense mutation (D678N) of amyloid precursor protein gene in
RT a Japanese pedigree of familial Alzheimer's disease.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB066441; BAB71958.1; -.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 4084 MW; 49D7D17289743B71 CRC64;

Query Match 81.8%; Score 36; DB 4; Length 35;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
   |||:||||
Db 12 SEVKMDAEF 20

RESULT 5
Q35463
ID Q35463 PRELIMINARY; PRT; 79 AA.
AC Q35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 79;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
   |||:||||
Db 16 SEVKMDAEF 24

RESULT 6
Q16014
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 81.8%; Score 36; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
   |||:||||
Db 13 SEVKMDAEF 21

RESULT 7
Q16019
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 81.8%; Score 36; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
   |||:||||
Db 13 SEVKMDAEF 21

RESULT 8
Q16020
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
```

DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
CN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -
DR HSSP: P05067; IBA4.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 81.8%; Score 36; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
Db 13 SEVKMDADF 21

RESULT 9
P78438
ID P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Amyloid protein (Beta-amyloid protein) (Fragment).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
similarity to soybean trypsin inhibitor";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
linkage near the Alzheimer locus";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Pavami H., Wajzman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
kindreds for the APP gene region";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL: M29270; AAA51768.1; -
DR EMBL: M29269; AAA51768.1; JOINED.
DR EMBL: M15532; AAA51564.1; -
DR EMBL: S45136; AAB23646.1; -
DR HSSP: P05067; IBA4.

DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 81.8%; Score 36; DB 4; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
Db 12 SEVKMDADF 20

RESULT 10
O93296
ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
substrate for caspase-3 in dying motoneurons";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1; -
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDAM.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E6D4C92 CRC64;

Query Match 81.8%; Score 36; DB 13; Length 534;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
Db 431 SEVKMDADF 439

RESULT 11
Q9PVL1
ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;

RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 81.8%; Score 36; DB 13; Length 569;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
DB 467 SEVKMDAEF 475
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RESULT 12
Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 68.4 kDa protein (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AA05490.1; -.
DR HSSP; P05067; 1AAP.
DR MCD; MGI-88059; AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 607;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
DB 504 SEVKMDAEF 512
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RESULT 13

Q95KN7 PRELIMINARY; PRT; 695 AA.
AC Q95KN7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Amyloid B-protein precursor.
OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; UNKNOWN_1.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 81.8%; Score 36; DB 6; Length 695;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
DB 592 SEVKMDAEF 600
||| :|||

RESULT 14

Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative amyloid precursor protein.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Mon Nov 18 17:35:36 2002

Query Match 81.8%; Score 36; DB 11; Length 695;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
|||:||||
DB 592 SEVKMDADF 600

RESULT 15

P97487
ID P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hippocampal amyloid protein.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=129SV;
RA Wrang M.A., Busfield F., Duff K., Korenblat K., Capeocchi M.,
RA Loring J.F., Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -;
DR EMBL; U82624; AAB40919.1; -;
DR HSSP; P05067; IMWP.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03454; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 81.8%; Score 36; DB 11; Length 695;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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DB 592 SEVKMDADF 600

Search completed: November 18, 2002, 12:53:33
Job time : 21.1739 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:51:08 ; Search time 8.6087 Seconds
(without alignments)
30.760 Million cell updates/sec

Title: US-09-724-571-83

Perfect score: 44

Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA:*
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2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	3	US-08-802-981-219
2	44	100.0	10	2	US-08-659-984A-19
3	44	100.0	10	4	US-08-660-531-19
4	44	100.0	10	4	US-09-548-372D-63
5	44	100.0	10	4	US-09-548-367D-63
6	44	100.0	11	5	PCT-US94-07043A-3
7	44	100.0	21	2	US-08-659-984A-18
8	44	100.0	21	3	US-08-660-531-18
9	44	100.0	30	2	US-08-659-984A-17
10	44	100.0	30	2	US-08-660-531-17
11	44	100.0	30	4	US-08-659-984A-16
12	44	100.0	33	2	US-08-660-531-16
13	44	100.0	33	4	US-08-659-984A-15
14	44	100.0	42	2	US-08-660-531-15
15	44	100.0	42	2	US-08-659-984A-21
16	44	100.0	506	2	US-08-659-984A-21
17	44	100.0	506	4	US-08-660-531-21
18	44	100.0	506	4	US-09-054-334-4
19	44	100.0	695	4	US-09-548-372D-12
20	44	100.0	695	4	US-09-548-367D-12
21	44	100.0	697	4	US-09-548-372D-18
22	44	100.0	697	4	US-09-548-367D-18
23	40	90.9	103	3	US-08-339-708A-12
24	39	88.6	27	1	US-08-141-324-12
25	39	88.6	27	1	US-08-541-302-12
26	38	86.4	9	3	US-08-802-981-220
27	38	86.4	9	3	US-08-802-981-223

28	38	86.4	21	3	US-08-802-981-113	Sequence 113, App
29	38	86.4	21	3	US-08-802-981-116	Sequence 116, App
30	36	81.8	9	3	US-08-802-981-221	Sequence 221, App
31	36	81.8	9	4	US-09-294-987-6	Sequence 6, Appl
32	36	81.8	10	2	US-08-025-321C-1	Sequence 1, Appl
33	36	81.8	10	4	US-09-548-372D-64	Sequence 64, Appl
34	36	81.8	10	4	US-09-548-367D-54	Sequence 7, Appl
35	36	81.8	11	5	PCT-US94-07043A-7	Sequence 64, Appl
36	36	81.8	12	5	PCT-US94-07043A-2	Sequence 2, Appl
37	36	81.8	16	5	PCT-US94-07043A-1	Sequence 1, Appl
38	36	81.8	21	3	US-08-802-981-114	Sequence 114, App
39	36	81.8	27	1	US-08-141-324-11	Sequence 11, Appl
40	36	81.8	27	1	US-08-541-902-11	Sequence 11, Appl
41	36	81.8	45	1	US-08-462-859A-5	Sequence 5, Appl
42	36	81.8	45	1	US-08-123-659A-5	Sequence 5, Appl
43	36	81.8	45	1	US-08-464-247A-5	Sequence 5, Appl
44	36	81.8	45	1	US-08-464-248A-5	Sequence 5, Appl
45	36	81.8	58	1	US-08-371-930-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-802-981-219
; Sequence 219, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-802-981-219

Query Match 100.0%; Score 44; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.9e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9

DB 1 SEVNLDAEF 9

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RESULT 2
US-08-659-984A-19
; Sequence 19, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: one-of(1)
; OTHER INFORMATION: /note= "N-terminal Ser is acetylated"
US-08-659-984A-19

Query Match 100.0%; Score 44; DB 2; Length 1
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 9; Conservative 0; Mismatches 0; Indels 0

QY 1 SEVNLDADF 9
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DB 1 SEVNLDADF 9

RESULT 3
US-08-660-531-19
; Sequence 19, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

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US-09-548-372D-63

Query Match	100.0%;	Score 44;	DB 4;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 0.0025;		
Matches	9; Conservative	0; Mismatches	0; Indels	

QY 1 SEVNLDAEF 9
| | | | | | | |
Db 1 SEVNLDAEF 9

RESULT 5

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US-09-548-367D-63
; Sequence 63, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-548-367D-63

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Query Match	100.0%	Score 44;	DB 4;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 0.0025;		
Matches	9;	Conservative 0;	Mismatches 0;	Indels

Qy	1 SEVNDAEF 9
Db	1 SEVNDAEF 9

RESULT 6

PCT-US94-07043A-3
; Sequence 3, Application PC/TUS9407043A
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
; Applicant: Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHESPIN D IS AN AMYLOIDOGENIC
; TITLE OF INVENTION: CATHESPIN D IS AN AMYLOIDOGENIC
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4800
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07043A
; FILING DATE: June 21, 1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/10889
 ; FILING DATE: November 12, 1993
 ; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/995,660
; FILING DATE: December 16, 1992
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: 07/880,914
/
/ FILING DATE: MAY 11, 1992
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Pamela A. Simonton
/
/ REGISTRATION NUMBER: 31,060
/
/ REFERENCE/DOCKET NUMBER: MTI 224.3
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: (203) 937-2340
/
/ TELEFAX: (203) 937-2795
/
/ INFORMATION FOR SEQ ID NO: 3:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 11 amino acids
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/ TYPE: amino acid
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/ TOPOLOGY: linear
/
PCT-US94-07043A-3

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Query Match 100.0%; Score 44; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels

QY 1 SEVNLDAEF 9
Db 2 SEVNLDAEF 1

RESULT 7

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US-08-659-984A-18
; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids

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;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-659-984A-18

Query Match 100.0%; Score 44; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 8
US-08-802-981-112
; Sequence 112, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-00030005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
US-08-802-981-112

Query Match 100.0%; Score 44; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
| | | | | | | | | |
Db 6 SEVNLDADF 14

RESULT 9
US-08-660-531-18
; Sequence 18, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M. S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-531-18

Query Match 100.0%; Score 44; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDADF 9
| | | | | | | | | |
Db 1 SEVNLDADF 9

RESULT 10
US-08-659-984A-17
; Sequence 17, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-17

Query Match 100.0%; Score 44; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
|||||
Db 22 SEVNLDAEF 30

RESULT 11
US-08-660-531-17
Sequence 17, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Kelm, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-531-17

Query Match 100.0%; Score 44; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
|||||
Db 22 SEVNLDAEF 30

RESULT 12
US-08-659-984A-16
Sequence 16, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-659-984A-16

Query Match 100.0%; Score 44; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SEVNLDADF 9
Db 13 SEVNLDADF 21

RESULT 13
US-08-660-531-16
; Sequence 16, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-659-984A-15

Query Match 100.0%; Score 44; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
Db 22 SEVNLDADF 30

RESULT 15
US-08-660-531-15
; Sequence 15, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-660-531-16

Query Match 100.0%; Score 44; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
Db 13 SEVNLDADF 21

RESULT 14
US-08-659-984A-15
; Sequence 15, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
```

ATTORNEY/AGENT INFORMATION:
 NAME: Heslin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15270-002210US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-660-531-15

Query Match 100.0%; Score 44; DB 4; Length 42;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEVNLDAEF 9
 Db 22 SEVNLDAEF 30

Search completed: November 18, 2002, 12:54:35
 Job time : 9.6087 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2002, 12:52:19 : Search time 5.47826 Seconds
(without alignments)
24.743 Million cell updates/sec

Title: US-09-724-571-83

Perfect score: 44

Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62

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Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA.*
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2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	44	100.0	9	10	US-09-896-874-8
2	44	100.0	9	10	US-09-896-139-8
3	44	100.0	9	10	US-09-895-843-8
4	44	100.0	10	9	US-09-795-903A-5
5	44	100.0	10	10	US-09-794-927-63
6	44	100.0	10	10	US-09-795-847-63
7	44	100.0	10	10	US-09-794-743-63
8	44	100.0	10	10	US-09-794-748-63
9	44	100.0	10	10	US-09-796-264-5
10	44	100.0	10	10	US-09-794-925-63
11	44	100.0	10	10	US-09-681-442-63
12	44	100.0	10	10	US-09-845-226-5
13	44	100.0	12	10	US-09-896-874-1
14	44	100.0	12	10	US-09-896-139-1
15	44	100.0	12	10	US-09-895-843-1
16	44	100.0	30	10	US-09-896-874-9
17	44	100.0	30	10	US-09-896-139-9
18	44	100.0	30	10	US-09-895-843-9
19	44	100.0	32	10	US-09-896-874-4

20	44	100.0	32	10	US-09-896-139-4	Sequence 4, Appli
21	44	100.0	32	10	US-09-895-843-4	Sequence 4, Appli
22	44	100.0	33	10	US-09-896-874-6	Sequence 6, Appli
23	44	100.0	33	10	US-09-896-139-6	Sequence 6, Appli
24	44	100.0	33	10	US-09-895-843-6	Sequence 6, Appli
25	44	100.0	695	10	US-09-794-927-12	Sequence 12, Appl
26	44	100.0	695	10	US-09-795-847-12	Sequence 12, Appl
27	44	100.0	695	10	US-09-794-743-12	Sequence 12, Appl
28	44	100.0	695	10	US-09-794-748-12	Sequence 12, Appl
29	44	100.0	695	10	US-09-794-925-12	Sequence 12, Appl
30	44	100.0	695	10	US-09-681-442-12	Sequence 12, Appl
31	44	100.0	697	10	US-09-794-927-18	Sequence 18, Appl
32	44	100.0	697	10	US-09-795-847-18	Sequence 18, Appl
33	44	100.0	697	10	US-09-794-743-18	Sequence 18, Appl
34	44	100.0	697	10	US-09-794-748-18	Sequence 18, Appl
35	44	100.0	697	10	US-09-794-925-18	Sequence 18, Appl
36	44	100.0	697	10	US-09-681-442-18	Sequence 18, Appl
37	36	81.8	9	12	US-10-016-717-6	Sequence 6, Appli
38	36	81.8	10	9	US-09-795-903A-4	Sequence 4, Appli
39	36	81.8	10	10	US-09-794-927-64	Sequence 64, Appl
40	36	81.8	10	10	US-09-795-847-64	Sequence 64, Appl
41	36	81.8	10	10	US-09-794-743-64	Sequence 64, Appl
42	36	81.8	10	10	US-09-794-748-64	Sequence 64, Appl
43	36	81.8	10	10	US-09-796-264-4	Sequence 4, Appli
44	36	81.8	10	10	US-09-794-925-64	Sequence 64, Appl
45	36	81.8	10	10	US-09-681-442-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-09-896-874-8
; Sequence 8, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-8

Query Match 100.0%; Score 44; DB 10; Length 9;
Best Local Similarity 100.0%; Pred NO. 8.1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9

Db 1 SEVNLDAEF 9

RESULT 2

US-09-896-139-8
; Sequence 8, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gallunas, Andrea
; APPLICANT: Hom, Roy

APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mailhaid, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.25USU4
CURRENT APPLICATION NUMBER: US/09/896,139
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/268,497
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/279,779
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/295,589
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-896-139-8

Query Match 100.0%; Score 44; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 3
US-09-895-843-8
Sequence 8, Application US/09895843
Patent No. US20020143177A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Fang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gallunas, Andrea
APPLICANT: Hom, Roy
APPLICANT: Jagodzinska, Barbara
APPLICANT: John, Varghese
APPLICANT: Mailhaid, Michel
APPLICANT: Pulley, Shon R.
APPLICANT: Tenbrink, Ruth E.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.41USU1
CURRENT APPLICATION NUMBER: US/09/895,843
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-895-843-8

Query Match 100.0%; Score 44; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 4
US-09-795-903A-5
Sequence 5, Application US/09795903A
Patent No. US20020164760A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Lin, Xinli
APPLICANT: Koelsch, Gerald
TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
FILE REFERENCE: OMRF 179
CURRENT APPLICATION NUMBER: US/09/795,903A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/604,608
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-795-903A-5

Query Match 100.0%; Score 44; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 5
US-09-794-927-63
Sequence 63, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
FILE REFERENCE: 28341/6280FG
CURRENT APPLICATION NUMBER: US/09/794,927
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881

us-09-724-571-83.rapb

Mon Nov 18 17:35:35 2002

US-09-794-748-63

Query Match 100.0%; Score 44; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 9

US-09-796-264-5
; Sequence 5, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-796-264-5

Query Match 100.0%; Score 44; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 10

US-09-794-925-63
; Sequence 63, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280HI
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23

;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 63
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-794-925-63

Query Match 100.0%; Score 44; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 11

US-09-681-442-63
; Sequence 63, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-681-442-63

Query Match 100.0%; Score 44; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 12

US-09-845-226-5
; Sequence 5, Application US/09845226
; Patent No. US20020115600A1

; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-845-226-5

Query Match 100.0%; Score 44; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 13
US-09-896-874-1
; Sequence 1, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-1

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Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 14
US-09-896-139-1
; Sequence 1, Application US/09896139

; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailalaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-139-1

Query Match 100.0%; Score 44; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9
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Db 1 SEVNLDADF 9

RESULT 15
US-09-895-843-1
; Sequence 1, Application US/09895843
; Patent No. US20020143177A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Mailalaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.41USU1
; CURRENT APPLICATION NUMBER: US/09/895,843
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT

Mon Nov 18 17:35:35 2002

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-895-843-1
Query Match      100.0%; Score 44; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDREF 9
   |||||
Db 1 SEVNLDREF 9
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Search completed: November 18, 2002, 12:54:55
Job time : 5.47826 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run On: November 18, 2002, 12:41:03 ; Search time 24.2609 Seconds
(without alignments)
49.432 Million cell updates/sec

Title: US-09-724-571-83
Perfect score: 44
Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	AAW82081	Fluorogenic protea
2	44	100.0	9	AAW82081	A peptide fragment
3	44	100.0	9	AAW82081	Substrate for beta
4	44	100.0	9	AAW82081	Protease indicator
5	44	100.0	9	AAW82081	Peptide #1 used as
6	44	100.0	9	AAW82081	Oligopeptide subst
7	44	100.0	9	AAW82081	Synthetic oligopep
8	44	100.0	9	AAW82081	Oligopeptide subst
9	44	100.0	9	AAW82081	Synthetic amyloid
10	44	100.0	10	AAW82081	Beta-secretase sub

11	44	100.0	10	AAW82081	Synthetic oligopep
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13	44	100.0	10	AAW82081	Human APP-Sw beta-
14	44	100.0	10	AAW82081	Human APP-Sw beta-
15	44	100.0	10	AAW82081	Human amyloid prec
16	44	100.0	10	AAW82081	Synthetic Asp2 rec
17	44	100.0	10	AAW82081	Human beta-amyloid
18	44	100.0	10	AAW82081	Human APP-Sw beta-
19	44	100.0	10	AAW82081	Peptide 5-5'SW, fo
20	44	100.0	10	AAW82081	Synthetic peptide
21	44	100.0	10	AAW82081	Swedish mutation p
22	44	100.0	10	AAW82081	Peptide #2 used as
23	44	100.0	10	AAW82081	Beta-secretase spe
24	44	100.0	10	AAW82081	Human APP Swedish
25	44	100.0	11	AAW82081	APP Swedish varian
26	44	100.0	11	AAW82081	Asp 1 substrate se
27	44	100.0	11	AAW82081	Asp2 substrate swe
28	44	100.0	12	AAW82081	Amyloid precursor
29	44	100.0	12	AAW82081	Biotinylated synth
30	44	100.0	12	AAW82081	APP substrate pept
31	44	100.0	13	AAW82081	Synthetic amyloid
32	44	100.0	13	AAW82081	Beta-secretase rel
33	44	100.0	16	AAW82081	Fluorescent substr
34	44	100.0	18	AAW82081	Human beta-amyloid
35	44	100.0	19	AAW82081	Beta-amyloid precu
36	44	100.0	20	AAW82081	Amyloid precursor
37	44	100.0	20	AAW82081	Fluorogenic protea
38	44	100.0	20	AAW82081	Beta-APP alpha-sec
39	44	100.0	20	AAW82081	Protease binding s
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44	44	100.0	21	AAW82081	Protease binding s
45	44	100.0	21	AAW82081	Peptide 5-16'SW, f

ALIGNMENTS

RESULT 1
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ID AAW82081 standard; peptide; 9 AA.
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AC AAW82081;
XX
DT 18-FEB-1999 (first entry)
XX
DE Fluorogenic protease indicator protease binding peptide #59.
XX
KW Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
KW conformation change.
OS Synthetic.
XX
PN WO9837226-A1.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-0503000.
XX
PR 20-FEB-1997; 97US-0802981.
XX
PA (ONCO-) ONCOIMMUNIN INC.
XX
PI Komoriya A, Packard BS;
XX
DR WPI; 1998-467579/40.
XX
PT New fluorogenic compositions - containing 2 fluorophores separated
PT by a peptide comprising a protease binding site, used for detecting
PT protease activity in samples.

PS Claim 4; Page 77; 90pp; English.

XX AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, polysaccharides, proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to a molecule can be used to enhance uptake by cells. The composition is composed of P = peptide comprising a protease binding site for the protease, F1, F2 peptides = fluorophores where F1 is attached to the amino terminal amino acid and S1, S2 peptides = when present, are attached to the carboxyl terminal amino acid and S1, S2 peptides = when present, are attached to the amino terminal amino acid, and S2, when present, is attached to the carboxyl terminal amino acid.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 2

ID AAB07874 standard; peptide; 9 AA.

XX AC AAB07874;

XX DT 14-NOV-2000 (first entry)

XX DE A peptide fragment derived from beta-amyloid precursor protein.

XX KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.

XX KW Homo sapiens.

XX OS WO200047618-A2.

XX PN 17-AUG-2000.

XX PD 10-FEB-2000; 2000WO-US03819.

XX PF 10-FEB-1999; 99US-Q119571.

XX PR 15-JUN-1999; 99US-0139172.

XX XX (ELAN-) ELAN PHARM INC.

XX PA Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M; Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L; WPI; 2000-533011/48.

XX PI Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.

XX PT Disclosure; Page 12; 121pp; English.

XX XX The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive

CC ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide derived from beta-amyloid precursor protein

CC SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 3

ID AAB07894 standard; Peptide; 9 AA.

XX AC AAB07894;

XX DT 14-NOV-2000 (first entry)

XX DE Substrate for beta-secretase enzyme.

XX KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.

XX KW Synthetic.

XX OS

XX PH Key

XX FT Cleavage-site 5..6

XX PN WO200047618-A2.

XX PD 17-AUG-2000.

XX XX 10-FEB-2000; 2000WO-US03819.

XX PR 10-FEB-1999; 99US-Q119571.

XX PR 15-JUN-1999; 99US-0139172.

XX PA (ELAN-) ELAN PHARM INC.

XX PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M; Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L; WPI; 2000-533011/48.

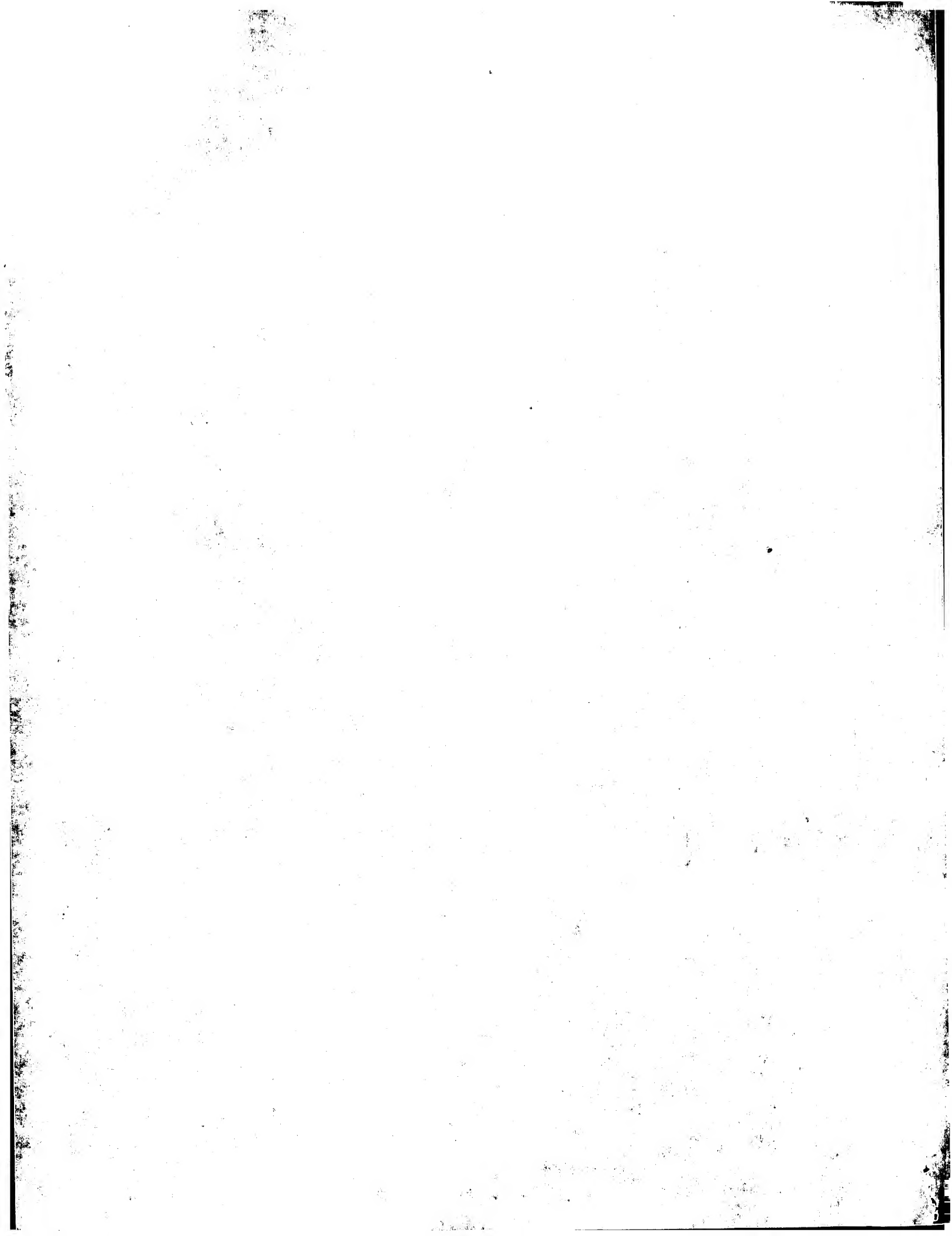
XX PT Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.

XX PT Example 4; Page 71; 121pp; English.

XX XX The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide substrate used to test the activity of beta-secretase enzyme.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:41:03 : Search time 24.2609 Seconds
(without alignments)
49.432 Million cell updates/sec

Title: US-09-724-571-83
Perfect score: 44
Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

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2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	19	AAW82081
2	44	100.0	9	21	AAW07874
3	44	100.0	9	21	AAW07894
4	44	100.0	9	22	AAG73297
5	44	100.0	9	23	ABW09003
6	44	100.0	9	23	AAW50897
7	44	100.0	9	23	ABW07598
8	44	100.0	9	23	AAW16663
9	44	100.0	9	23	AAU74837
10	44	100.0	10	18	AAW08362

11	44	100.0	10	20	AAW33756
12	44	100.0	10	21	AAW69707
13	44	100.0	10	22	AAE10653
14	44	100.0	10	22	AAE06898
15	44	100.0	10	22	AAU06627
16	44	100.0	10	22	AAU07226
17	44	100.0	10	22	AAE02605
18	44	100.0	10	22	AAW47266
19	44	100.0	10	22	AAW66575
20	44	100.0	10	22	AAW61337
21	44	100.0	10	23	AAU99491
22	44	100.0	10	23	ABW78614
23	44	100.0	10	23	ABW06425
24	44	100.0	11	22	AAW75142
25	44	100.0	11	22	AAW75145
26	44	100.0	11	22	AAW97469
27	44	100.0	12	23	ABW08996
28	44	100.0	12	23	ABW07591
29	44	100.0	12	23	AAE16656
30	44	100.0	12	23	AAU74830
31	44	100.0	13	23	ABW06591
32	44	100.0	13	23	AAW50890
33	44	100.0	16	21	AAW06316
34	44	100.0	18	22	AAE00609
35	44	100.0	19	22	AAE00611
36	44	100.0	20	19	AAW82211
37	44	100.0	20	21	AAW69714
38	44	100.0	20	22	AAW73229
39	44	100.0	20	23	AAW78509
40	44	100.0	21	18	AAW08361
41	44	100.0	21	19	AAW82186
42	44	100.0	21	20	AAW33755
43	44	100.0	21	22	AAW73203
44	44	100.0	21	22	AAW73204
45	44	100.0	21	22	AAW47265

ALIGNMENTS

RESULT 1
AAW82081
ID AAW82081 standard; peptide; 9 AA.
AC AAW82081;
DT 18-FEB-1999 (first entry)
DE Fluorogenic protease indicator protease binding peptide #59.
KW Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
KW conformation change.
OS Synthetic.
PN WO9837226-A1.
XX 27-AUG-1998.
XX 20-FEB-1998; 98WO-US03000.
XX 20-FEB-1997; 97US-0802981.
XX (ONCO-) ONCOIMMUNIN INC.
XX Komoriya A, Packard BS;
XX WPI; 1998-467579/40.
XX New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease activity in samples.

Synthetic oligopep
Beta-APP alpha-sec
Human APP-Sw beta-
Human amyloid prec
Synthetic Asp2 rec
Human beta-amyloid
Human APP-Sw beta-
Peptide 5-5'SW, fo
Synthetic peptide
Swedish mutation p
Peptide #2 used as
Beta-secretase spe
Human APP Swedish
APP Swedish varian
Asp2 substrate se
Asp2 substrate Sw
Amyloid precursor
Biotinylated synth
APP substrate pept
Synthetic amyloid
Beta-secretase rel
Fluorescent subst
Human beta-amyloid
Beta-amyloid precu
Amyloid precursor
Fluorogenic protea
Beta-APP alpha-sec
Protease binding s
Beta amyloid precu
Beta-secretase sub
Fluorogenic protea
Synthetic oligopep
Protease binding s
Protease binding s
Peptide 5-16'SW, f

PS Claim 4; Page 77; 90pp; English.

XX AAM82023-W82240 are peptides used in the construction of a fluorogenic

CC composition which is used for the detection of protease activity in

CC biological samples. The products can be used for the detection of

CC conformational changes in nucleic acids, oligosaccharides,

CC polysaccharides, proteins, peptides, lipids, phospholipids, glycolipids,

CC glycoproteins, steroids or polymers. In addition, attachment of a

CC hydrophobic group to a molecule can be used to enhance uptake by cells.

CC The composition is composed of P = peptide comprising a protease binding

CC site for the protease, F1, F2 peptides = fluorophores where F1 is

CC attached to the amino terminal amino acid and F2 is attached to the

CC carboxyl terminal amino acid and S1, S2 peptides = when present, are

CC peptide spacers where S1, when present, is attached to the amino terminal

CC acid, and S2, when present, is attached to the carboxyl terminal amino

CC acid.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9

Db 1 SEVNLDADF 9

RESULT 2

AAB07874

ID AAB07874 standard; peptide; 9 AA.

XX

AC AAB07874;

XX

DT 14-NOV-2000 (first entry)

XX

DE A peptide fragment derived from beta-amyloid precursor protein.

XX

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor.

XX

OS Homo sapiens.

XX

XX WO200047618-A2.

PN

XX

PD 17-AUG-2000.

PF

XX

XX 10-FEB-2000; 2000WO-US03819.

PR

XX

PR 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX

XX (ELAN-) ELAN PHARM INC.

PA

XX

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

PI

XX

DR WPI; 2000-533011/48.

XX

XX Purified beta-secretase protein used in assays to discover inhibitors

PT which can be used for the treatment of amyloidogenic diseases e.g.

PT Alzheimer's disease -

XX

XX Disclosure; Page 12; 121pp; English.

PS

XX

XX The specification describes a beta-secretase enzyme. The enzyme cleaves

CC beta-amyloid precursor protein to produce beta-amyloid peptide. This

CC enzyme is therefore implicated in the production of amyloid plaque

CC components which accumulate in the brains of individuals afflicted with

CC Alzheimer's disease. Inhibitors of beta-secretase are administered to

CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's

CC disease-like pathology to test if they maintain or improve cognitive

CC

CC ability or reduce the plaque burden. The compounds are used for the

CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The

CC present sequence represents a peptide substrate used to test the

CC activity of beta-secretase enzyme.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9

Db 1 SEVNLDADF 9

RESULT 3

AAB07894

ID AAB07894 standard; Peptide; 9 AA.

XX

XX AAB07894;

AC

XX

DT 14-NOV-2000 (first entry)

XX

DE Substrate for beta-secretase enzyme.

XX

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FH Cleavage-site 5..6

FT

XX

XX WO200047618-A2.

PN

XX

PD 17-AUG-2000.

XX

XX 10-FEB-2000; 2000WO-US03819.

XX

XX 10-FEB-1999; 99US-0119571.

PR

XX

PR 15-JUN-1999; 99US-0139172.

XX

XX (ELAN-) ELAN PHARM INC.

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XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

PI

XX

DR WPI; 2000-533011/48.

XX

XX Purified beta-secretase protein used in assays to discover inhibitors

PT which can be used for the treatment of amyloidogenic diseases e.g.

PT Alzheimer's disease -

XX

XX Example 4; Page 71; 121pp; English.

PS

XX

XX The specification describes a beta-secretase enzyme. The enzyme cleaves

CC beta-amyloid precursor protein to produce beta-amyloid peptide. This

CC enzyme is therefore implicated in the production of amyloid plaque

CC components which accumulate in the brains of individuals afflicted with

CC Alzheimer's disease. Inhibitors of beta-secretase are administered to

CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's

CC disease-like pathology to test if they maintain or improve cognitive

CC ability or reduce the plaque burden. The compounds are used for the

CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The

CC present sequence represents a peptide substrate used to test the

CC activity of beta-secretase enzyme.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

PS Claim 4; Page 77; 90pp; English.

XX AAM82023-W82240 are peptides used in the construction of a fluorogenic

CC composition which is used for the detection of protease activity in

CC biological samples. The products can be used for the detection of

CC conformational changes in nucleic acids, oligosaccharides,

CC polysaccharides, proteins, peptides, lipids, phospholipids, glycolipids,

CC glycoproteins, steroids or polymers. In addition, attachment of a

CC hydrophobic group to a molecule can be used to enhance uptake by cells.

CC The composition is composed of P = peptide comprising a protease binding

CC site for the protease, F1, F2 peptides = fluorophores where F1 is

CC attached to the amino terminal amino acid and F2 is attached to the

CC carboxyl terminal amino acid and S1, S2 peptides = when present, are

CC peptide spacers where S1, when present, is attached to the amino terminal

CC acid, and S2, when present, is attached to the carboxyl terminal amino

CC acid.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDADF 9

Db 1 SEVNLDADF 9

RESULT 2

AAB07874

ID AAB07874 standard; peptide; 9 AA.

XX

AC AAB07874;

XX

DT 14-NOV-2000 (first entry)

XX

DE A peptide fragment derived from beta-amyloid precursor protein.

XX

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

KW inhibitor.

XX

OS Homo sapiens.

XX

XX WO200047618-A2.

PN

XX

PD 17-AUG-2000.

PF

XX

XX 10-FEB-2000; 2000WO-US03819.

PR

XX

PR 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX

XX (ELAN-) ELAN PHARM INC.

PA

XX

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

PI

XX

DR WPI; 2000-533011/48.

XX

XX Purified beta-secretase protein used in assays to discover inhibitors

PT which can be used for the treatment of amyloidogenic diseases e.g.

PT Alzheimer's disease -

XX

XX Disclosure; Page 12; 121pp; English.

PS

XX

XX The specification describes a beta-secretase enzyme. The enzyme cleaves

CC beta-amyloid precursor protein to produce beta-amyloid peptide. This

CC enzyme is therefore implicated in the production of amyloid plaque

CC components which accumulate in the brains of individuals afflicted with

CC Alzheimer's disease. Inhibitors of beta-secretase are administered to

CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's

CC disease-like pathology to test if they maintain or improve cognitive

CC

CC ability or reduce the plaque burden. The compounds are used for the

CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The

CC present sequence represents a peptide substrate used to test the

CC activity of beta-secretase enzyme.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDAEF 9
 |||||
 Db 1 SEVNLDAEF 9

RESULT 4
 AAG73297
 ID AAG73297 standard; Peptide; 9 AA.
 XX AC AAG73297;
 XX DT 14-AUG-2001 (first entry)
 XX DE
 XX DE Protease indicator compound peptide #26.
 XX DE
 KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
 KW viral infection; cancer metastasis; emphysema; arthritis;
 KW thrombosis; haemophilia.
 XX OS Synthetic.
 XX PN WO200118238-A1.
 XX PD 15-MAR-2001.
 XX PF 11-SEP-2000; 2000WO-US24882.
 XX PR 10-SEP-1999; 99US-0394019.
 XX PA (ONCO-) ONCOIMMUNIN INC.
 XX PI Komoriya A, Packard BS;
 XX DR WPI; 2001-389573/41.
 XX PT New fluorogenic compositions whose fluorescence level increases in the
 PT presence of active proteases, useful for detecting and localizing
 PT protease activity in biological samples, particularly in frozen tissue
 PT samples -
 XX PS Claim 1; Page 70; 86pp; English.
 XX CC The present invention describes fluorogenic compositions which can be
 CC used for the detection of protease activity. This can be useful as an
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
 CC thrombosis and arthritis. The fluorogenic compositions comprise a
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
 CC peptide is cleaved by a protease and the fluorophores can then be
 CC detected. The present sequence is one of the peptides described in the
 CC exemplification of the invention.
 XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDAEF 9
 |||||
 Db 1 SEVNLDAEF 9

RESULT 5
 ABB09003
 ID ABB09003 standard; peptide; 9 AA.
 XX AC ABB09003;
 XX DT 19-JUN-2002 (first entry)
 XX DE Peptide #1 used as a tag to identify cleavage products.

XX Amyloid precursor protein; APP; Alzheimer's disease; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;
 KW Down's syndrome; cerebral amyloid angiopathy; dementia.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Cleavage-site 5..6
 FT /note= "Beta secretase cleavage site"
 XX WO200202505-A2.
 XX PD 10-JAN-2002.
 XX PF 29-JUN-2001; 2001WO-US20852.
 XX PR 30-JUN-2000; 2000US-215323P.
 XX PA (ELAN-) ELAN PHARM INC.
 XX PI Fang LY, Hom R, John V, Maillaird M;
 XX WPI; 2002-171625/22.
 XX DR New substituted amines are e.g. beta-amyloid peptide inhibitors, useful
 PT for treating Alzheimer's disease, mild cognitive impairment and Down's
 PT syndrome -
 XX PS Example D; Page 96; 136pp; English.
 XX CC This invention relates to substituted amines and their salts, which
 CC are neurotropic, neuroprotective, cerebroprotective, haemostatic and
 CC antiparkinsonian in their action. They are used in the preparation of
 CC a composition useful for treating, preventing or delaying the on-set
 CC of Alzheimer's disease, for treating mild cognitive impairment, Down's
 CC syndrome, cerebral amyloid angiopathy, dementia associated with
 CC parkinson's disease, dementia associated with progressive supranuclear
 CC palsy, and dementia associated with cortical basal degeneration.
 CC They are also useful for treating diseases characterised by beta-amyloid
 CC deposits in brain, and for producing beta-secretase complexes. This
 CC sequence represents a peptide that incorporate the known cleavage
 CC site of beta-secretase. This substrate is used to assay
 CC beta-secretase activity.
 XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEVNLDAEF 9
 |||||
 Db 1 SEVNLDAEF 9

RESULT 6
 AAM50897
 ID AAM50897 standard; Peptide; 9 AA.
 XX AC AAM50897;
 XX DT 07-MAY-2002 (first entry)
 XX DE Oligopeptide substrate for beta-secretase.
 XX DE
 KW Beta-secretase; substrate; amyloid precursor protein;
 KW APP; amyloid beta peptide; inhibitor; screening;
 KW neurodegenerative disorder; cognitive impairment; Down's syndrome;
 KW Alzheimer's disease; hereditary cerebral haemorrhage;
 KW cerebral amyloid angiopathy; dementia; therapy.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Cleavage-site 5..6
XX PN WO200202512-A2.
XX PD 10-JAN-2002.
XX PF 29-JUN-2001; 2001WO-US21012.
XX PR 30-JUN-2000; 2000US-215323P.
XX PR 22-NOV-2000; 2000US-252736P.
XX PR 15-DEC-2000; 2000US-253956P.
XX PR 13-FEB-2001; 2001US-268497P.
XX PR 29-MAR-2001; 2001US-279779P.
XX PR 04-JUN-2001; 2001US-295589P.
XX PA (ELAN-) ELAN PHARM INC.
XX PA (PHAA) PHARMACIA & UPJOHN CO.
XX PI Maillaird M, Hom C, Gailunas A, Jagodzinska B, Fang LY, John V;
XX PI Freskos JN, Pulley SR, Beck JP, Tenbrink RE;
XX DR . WPI; 2002-171627/22.
XX PT New substituted amines are e.g. amyloid beta peptide production
XX PT inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
XX PT mild cognitive impairment and other degenerative diseases -
XX PS Example D; Page 344; 651pp; English.
XX CC The present sequence is that of a peptide that incorporates the
XX CC known cleavage site of beta-secretase on amyloid precursor protein
XX CC (APP). The peptide, which may optionally be tagged with a
XX CC fluorescent or chromogenic moiety, can be used in assays to
XX CC determine the beta-secretase inhibitory activity of novel
XX CC substituted amine compounds of the invention. Comparison of
XX CC substrate cleavage results in the presence of an inhibitor and
XX CC in the presence of a control provides a measure of the compound's
XX CC inhibitory activity. Novel compounds of the invention are
XX CC effective inhibitors of beta-secretase, inhibit beta-secretase
XX CC mediated cleavage of APP, are effective inhibitors of A beta
XX CC production, and/or effectively reduce amyloid beta deposits or
XX CC plaques. They are used in the treatment or prevention of diseases
XX CC characterised by amyloid deposits in the brain, e.g. for treating
XX CC or preventing Alzheimer's disease (AD), for helping prevent or
XX CC delay the onset of AD, for treating mild cognitive impairment
XX CC (MCI), preventing or delaying the onset of AD in those who would
XX CC progress from MCI to AD, for treating Down's syndrome and
XX CC hereditary cerebral haemorrhage with Amyloidosis of the Dutch
XX CC type, for treating cerebral amyloid angiopathy and preventing its
XX CC potential consequences i.e. single and recurrent lobar haemorrhages,
XX CC for treating other degenerative dementias, including dementias
XX CC of mixed vascular and degenerative origin, dementia associated with
XX CC Parkinson's disease, dementia associated with progressive
XX CC supranuclear palsy, and dementia associated with cortical basal
XX CC degeneration, and for treating diffuse Lewy body type of AD (all
XX CC claimed).

XX SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9
RESULT 7
ABB07598
ID ABB07598 standard; peptide; 9 AA.

XX ABB07598;
XX AC
XX DT 08-MAY-2002 (first entry)
XX PN Synthetic oligopeptide substrate having beta-secretase cleavage site.
XX DE APP; amine derivative; beta-secretase; amyloid precursor protein; A beta;
XX KW amyloid beta peptide; beta-amyloid; nootropic; neuroprotective;
XX KW cerebroprotective; haemostatic; antiparkinsonian.
XX OS Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX XX Cleavage-site 5..6 /note= "beta-secretase cleavage site"
XX FT
XX FT
XX PN WO200202520-A2.
XX PN
XX XX 10-JAN-2002.
XX PD
XX XX 02-JUL-2001; 2001WO-US21000.
XX PF
XX XX 30-JUN-2000; 2000US-215323P.
XX PR 29-JUN-2001; 2001US-0895843.
XX XX (ELAN-) ELAN PHARM INC.
XX PA (PHAA) PHARMACIA & UPJOHN CO.
XX PA
XX PI Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;
XX PI WPI; 2002-188416/24.
XX DR
XX PT New substituted amine derivatives, useful for treating Alzheimer's
XX PT disease and other degenerative diseases -
XX PS Example D; Page 163; 286pp; English.
XX CC The invention relates to substituted amine derivatives of specified
XX CC formulae or their salts. The amine derivatives can inhibit beta-secretase
XX CC activity or inhibit the cleavage of amyloid precursor protein (APP) in a
XX CC reaction mixture. They can also be used to inhibit production of amyloid
XX CC beta peptide (A beta) in a cell or inhibit production of beta-amyloid
XX CC plaque in an animal. The amine derivatives are useful for treating or
XX CC preventing a disease characterized by beta-amyloid deposits in the brain
XX CC e.g. for treating or preventing Alzheimer's disease (AD), for helping
XX CC prevent or delay the onset of AD, for treating mild cognitive impairment
XX CC (MCI), preventing or delaying the onset of AD in those who would progress
XX CC from MCI to AD, for treating Down's syndrome, humans who have hereditary
XX CC cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
XX CC amyloid angiopathy and preventing its potential consequences i.e. single
XX CC and recurrent lobar haemorrhages, for treating other degenerative
XX CC dementias, including dementias of mixed vascular and degenerative origin,
XX CC dementia associated with Parkinson's disease, dementia associated with
XX CC progressive supranuclear palsy, dementia associated with cortical basal
XX CC degeneration, diffuse Lewy body type of Alzheimer's disease. Sequences
XX CC ABB07598-599 are synthetic APP oligopeptide substrates containing the
XX CC cleavage site of beta-secretase, used to assay beta-secretase activity.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9
RESULT 8
AAE16663
ID AAE16663 standard; peptide; 9 AA.

XX AC AAEL6663;
XX DT 09-APR-2002 (first entry)
XX DE Oligopeptide substrate #1, used in the assay of the invention.
XX KW Disubstituted amine derivative; Alzheimer's disease; Down's syndrome;
KW degenerative disease; beta-amyloid deposit; mild cognitive impairment;
KW hereditary cerebral haemorrhage; amyloidosis; degenerative dementia;
KW cerebral amyloid angiopathy; Parkinson's disease; supranuclear palsy;
KW cortical basal degeneration; AD; MCI; amyloid precursor protein;
KW beta-secretase; amyloid beta peptide; A beta peptide.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Cleavage-site 5..6
XX PN WO200202518-A2.
XX PD 10-JAN-2002.
XX PF 29-JUN-2001; 2001WO-US20856.
XX PR 30-JUN-2000; 2000US-215323P.
XX PA (ELAN-) ELAN PHARM INC.
XX PH (PHAA) PHARMACIA & UPJOHN CO.
XX PI Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;
XX DR WPI; 2002-122550/16.
XX DT New substituted amine derivatives, useful for treating Alzheimer's
XX PT disease and other degenerative diseases -
XX PS Example D; Page 163; 286pp; English.
XX CC The invention relates to disubstituted amine derivative compounds
CC useful for treating Alzheimer's disease and other degenerative diseases.
CC Compounds of the invention possess beta secretase inhibitory activity and
CC are useful for inhibiting beta-secretase mediated cleavage of amyloid
CC precursor protein (APP) and particularly, to inhibit the production of
CC amyloid beta (A beta) peptide. They are useful for treating or preventing
CC a disease characterised by beta-amyloid deposits in the brain e.g. for
CC treating or preventing Alzheimer's disease (AD), for helping to prevent
CC or delay the onset of Alzheimer's disease (AD), for helping to prevent
CC impairment (MCI), Down's syndrome, hereditary cerebral haemorrhage with
CC the amyloidosis of the Dutch type, cerebral amyloid angiopathy and
CC preventing its potential consequences i.e. single and recurrent lobar
CC haemorrhages, for treating other degenerative dementias including
CC dementias of mixed vascular and degenerative dementias associated
CC with Parkinson's disease, dementia associated with progressive
CC supranuclear palsy, dementia associated with cortical basal degeneration
CC and diffuse Lewy body type of Alzheimer's disease. The present sequence
XX is oligopeptide substrate used in assay of the invention.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLD AEF 9
Db 1 SEVNLD AEF 9
|||||||
RESULT 9
AAU74837
ID AAU74837 standard; Peptide; 9 AA.
XX

AC AAU74837;
XX DT 09-APR-2002 (first entry)
XX DE Synthetic amyloid precursor protein (APP) oligopeptide substrate #1.
XX KW Amyloid precursor protein; APP; Alzheimer's disease; amine XV;
KW neurotropic; neuroprotective; cerebroprotective; haemostatic;
KW antiparkinsonian; beta-secretase; amyloid beta peptide; amyloidosis;
KW beta-amyloid plaque; mild cognitive impairment; MCI; Down's syndrome;
KW hereditary cerebral haemorrhage; cortical basal degeneration;
KW cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;
KW Parkinson's disease; supranuclear palsy; dementia.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Cleavage site 5..6
XX PN /note- "Beta-secretase cleavage site"
XX PD WO200202506-A2.
XX PF 10-JAN-2002.
XX PR 29-JUN-2001; 2001WO-US20930.
XX PA 30-JUN-2000; 2000US-215323P.
XX PI (ELAN-) ELAN PHARM INC.
XX PI Fang LY, John V;
XX DR WPI; 2002-147995/19.
XX DT New substituted amines are e.g. amyloid beta peptide production
XX PT inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
XX PS mild cognitive impairment and other degenerative diseases -
XX PS Example D; Page 118; 434pp; English.
XX CC This invention relates to a novel substituted amine of formula XV and
CC its salts which can be used to treat Alzheimer's disease and similar
CC diseases. The compound of the invention may have neurotropic,
CC neuroprotective, cerebroprotective, haemostatic and antiparkinsonian
CC activities. The amine acts as a beta-secretase activity inhibitor,
CC inhibiting cleavage of amyloid precursor protein (APP) and the
CC formation of amyloid beta peptide and beta-amyloid plaque production.
CC The amine of the invention is useful for treating or preventing a
CC disease characterised by beta-amyloid deposits in the brain e.g.
CC Alzheimer's disease (AD), for treating mild cognitive impairment (MCI),
CC preventing or delaying the onset of Alzheimer's disease in those who
CC would progress from MCI to AD, for treating Down's syndrome, humans who
CC have hereditary cerebral haemorrhage with the Amyloidosis of the Dutch
CC type, cerebral amyloid angiopathy and preventing its potential
CC consequences i.e. single and recurrent lobar haemorrhages, for treating
CC other degenerative dementias, including dementias of mixed vascular and
CC degenerative origin, dementia associated with Parkinson's disease,
CC dementia associated with progressive supranuclear palsy, dementia
CC associated with cortical basal degeneration and diffuse Lewy body type
CC of Alzheimer's disease. The present sequence represents a synthetic
CC APP oligopeptide substrate #1 for the beta secretase enzyme. This
CC synthetic substrate was used to test the efficiency of the amine as an
CC inhibitor of beta secretase enzyme activity.
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLD AEF 9
Db 1 SEVNLD AEF 9
|||||||

Mon Nov 18 17:35:34 2002

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XX AC AAY33756;
XX DT 09-NOV-1999 (first entry)
XX DE Synthetic oligopeptide 5-5'SW.
XX KW Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
XX KW Alzheimer's disease; measure activity; cleavage site.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal Ser is acetylated"
XX PN US5942400-A.
XX PD 24-AUG-1999.
XX PF 07-JUN-1996; 96US-0659984.
XX PR 07-JUN-1996; 96US-0659984.
XX PR 07-JUN-1995; 95US-0480498.
XX PR 07-JUN-1995; 95US-0485152.
XX PA (ELAN-) ELAN PHARM INC.
XX PI Anderson JP, Jacobson-Croak KL, Sinha S;
XX DR WPI; 1999-517417/43.
XX PT A method for detecting human beta-secretase cleavage of polypeptides
XX PT useful for identifying beta-secretase inhibitors
XX PS Examples; Column 30; 43pp; English.
XX CC Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
XX CC the activity of beta-secretase (AAY33741). Beta-secretase is capable of
XX CC cleaving beta-amyloid protein precursor (APP) (AAY33742). These
XX CC synthetic peptides contain the cleavage site of APP. Beta-secretase and
XX CC APP are used in a method for detecting human beta-secretase cleavage of
XX CC polypeptides and for identifying beta-secretase inhibitors. Inhibition
XX CC of beta-secretase activity would be useful for chemical modelling of a
XX CC critical event in the pathology of Alzheimer's disease. Inhibitors of
XX CC beta-secretase would be useful for the prevention and treatment of
XX CC Alzheimer's disease and Down's Syndrome.
XX SQ Sequence 10 AA;
    Query Match 100.0%; Score 44; DB 20; Length 10;
    Best Local Similarity 100.0%; Pred. No. 0.0087;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLDADF 9
Db 1 SEVNLDADF 9
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RESULT 12
AAY69707
ID AAY69707 standard; peptide; 10 AA.
XX AC AAY69707;
XX DT 11-APR-2000 (first entry)
XX DE Beta-APP alpha-secretase substrate [NLD]-APP(-5,+5).
XX KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
XX KW cleavage site; beta-secretase; neurodegenerative disease;
XX KW Alzheimer's disease.
XX

RESULT 10
AAW08362
ID AAW08362 standard; peptide; 10 AA.
XX AC AAW08362;
XX DT 05-SEP-1997 (first entry)
XX DE Beta-secretase substrate #3.
XX KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
XX KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Misc-difference 1
XX FT /note= "acetylated"
XX PN W09640885-A2.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US09985.
XX PR 07-JUN-1995; 95US-0485152.
XX PR 07-JUN-1995; 95US-0480498.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
XX PI Mcconlogue LC, Sinha S, Tan H;
XX DR WPI; 1997-052304/05.
XX PT Beta-secretase which specifically cleaves beta-amyloid precursor
XX PT protein - useful to screen for inhibitors useful in treatment of
XX PT Alzheimer's disease
XX PS Disclosure; Page 45; 92pp; English.
XX CC AAW08359-W08362 represent substrates for the enzyme of the invention.
XX CC The enzyme of the invention is beta-secretase, and specifically cleaves
XX CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP
XX CC is thought to occur via cleavage between residues 16 and 17 of the
XX CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing
XX CC is thought to occur by beta-secretase cleavage of beta-APP.
XX CC Beta-secretase activity can be detected and measured using a method of
XX CC the invention, which detects at least one of the beta-secretase cleavage
XX CC products formed on cleavage. The method can be used to determine whether
XX CC a test substance inhibits proteolytic cleavage, by beta-secretase, of
XX CC beta-APP. Compounds effective to at least partially inhibit
XX CC beta-secretase activity can be used to inhibit cleavage of beta-APP in
XX CC cells or mammalian hosts. Isolation and purification of beta-secretase
XX CC will permit chemical modelling of a critical event in the pathology of
XX CC Alzheimer's disease.
XX SQ Sequence 10 AA;
    Query Match 100.0%; Score 44; DB 18; Length 10;
    Best Local Similarity 100.0%; Pred. No. 0.0087;
    Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEVNLDADF 9
Db 1 SEVNLDADF 9
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RESULT 11
AAY33756
ID AAY33756 standard; Protein; 10 AA.
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OS Homo sapiens.
OS Synthetic.

XX WO9964587-A1

XX 16-DEC-1999.

XX 04-JUN-1999; 99WO-FR01326.

XX 05-JUN-1998; 98FR-0007068.

XX 31-MAR-1999; 99US-0122599.

XX (RHON) RHONE-POULENC RORER SA.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
PI WPI; 2000-097537/08.

XX Polypeptide with beta-secretase activity, specific for wild-type

PT amyloid precursor protein, useful in treating Alzheimer's disease -
XX Example 3; Page 24; 44pp; French.

XX Peptides AAY69702-V69718 represent synthetic peptide substrates for a

CC novel polypeptide with beta-secretase activity that can cleave
CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
CC cleavage of the protein occurs between amino acids Met596-Asp597 and
CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel
CC polypeptide is used to identify agents that interact specifically with
CC it. These agents regulate metabolism of APP, particularly they slow down
CC or reduce production of beta-amyloid, so can be used to treat
CC neurodegenerative diseases, particularly Alzheimer's disease.

XX Sequence 10 AA;

Query Match 100.0%; Score 44; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLD AEF 9

Db 1 SEVNLD AEF 9

RESULT 13

AAE10653
ID AAE10653 standard; peptide; 10 AA.

XX AAE10653;

XX 10-DEC-2001 (first entry)

XX Human APP-Sw beta-secretase substrate peptide mutant, PHA-247574E.

XX Human; aspartyl protease 1; Aspl; amyloid precursor protein;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective;
KW APP-Sw beta-secretase peptide; mutant; mutin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 4 /note= "Wild type Lys substituted with Asn"

XX Misc-difference 5 /note= "Wild type Met substituted with Leu"

XX Cleavage-site 5..6

XX GB2357767-A.

XX 04-JUL-2001.

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22-SEP-2000; 2000GB-0023315.

23-SEP-1999; 99US-0155493.

23-SEP-1999; 99US-0404133.

23-SEP-1999; 99WO-US20881.

13-OCT-1999; 99US-0416901.

06-DEC-1999; 99US-0169232.

(PHAA) PHARMACIA & UPJOHN CO.

Bienkowski MJ, Gurney M;

WPI; 2001-444208/48.

Polypeptide comprising fragments of human aspartyl protease with
amyloid precursor protein processing activity and alpha-secretase
activity, for identifying modulators useful in treating Alzheimer's
disease -

Example 12; Page 84; 187pp; English.

The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
Aspl proteins which lack transmembrane domain or amino terminal
domain or cytoplasmic domain and retains alpha-secretase activity
and amyloid protein precursor (APP) processing activity. The proteins
of the invention are useful for assaying hu-Aspl alpha-secretase
activity, which in turn is useful for identifying modulators of
hu-Aspl alpha-secretase activity, where modulators that increase
hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
disease (AD) which causes progressive dementia with consequent
formation of amyloid plaques, neurofibrillary tangles, gliosis and
neuronal loss. Hu-Aspl protease substrate is useful for assaying
the substrate proteolytic activity, by contacting hu-Aspl protein with
hu-Aspl proteolytic activity. The present sequence is human amyloid
precursor protein-Swedish (APP-Sw) beta-secretase specific substrate
peptide mutant, PHA-247574E. This peptide is obtained by Swedish
KM-NL mutation. This peptide is used for assaying the beta-secretase
activity of human Aspartyl protease 2a (Asp2a) protein. The peptide
is also used for determining the relationship between Aspl and
APP protein.

XX Sequence 10 AA;

Query Match 100.0%; Score 44; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLD AEF 9

Db 1 SEVNLD AEF 9

RESULT 14

AAE06898

ID AAE06898 standard; peptide; 10 AA.

XX AAE06898;

XX 23-OCT-2001 (first entry)

XX Human amyloid precursor protein (APP-Sw) beta-secretase peptide #1.

XX Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
KW neuroprotective; antisense therapy; App-Sw; gene therapy.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

XX Cleavage-site 5..6

/label= Asp2_protease_cleavage_site

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XX WO200150829-A2.
XX 19-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00799.
XX 09-MAY-2001; 2001WO-IB00799.
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-483072/52.
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity -
XX Claim 10; Page 84; 185pp; English.
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease,
XX dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
XX and neuronal loss. APP isoforms are also used in methods for identifying
XX inhibitors and modulators of human Asp2 activity. The invention relates
XX to a method for identifying agents that modulate the activity of human
XX aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
XX as a means to screen in cellular assays for the inhibitors of beta- and
XX gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
XX polymerase chain reactions (PCR). The probes are useful for detecting
XX Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
XX blots. The present sequence is human amyloid precursor protein (APP-Sw)
XX beta-secretase peptide related to the invention.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 44; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.0087;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SEVNLDADF 9
XX | | | | | | | |
XX Db 1 SEVNLDADF 9
XX RESULT 15
XX AAU06627
XX ID AAU06627 standard; Peptide; 10 AA.
XX AC AAU06627;
XX XX
XX 24-OCT-2001 (first entry)
XX DE Synthetic Asp2 recognition site from APP-SW.
XX KW Aspartyl protease; Asp2; beta-secretase; nootropic;
XX KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
XX KW amyloid-beta; Abeta; APP-SW.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Cleavage-site 5

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FT /label= Asp2_protease_cleavage_site
XX WO200149098-A2.
XX 12-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00798.
XX 09-MAY-2001; 2001WO-IB00798.
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-502549/55.
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity -
XX Claim 10; Page 84; 185pp; English.
XX The invention relates to a purified polypeptide comprising a fragment of
XX mammalian aspartyl protease (Asp2) protein which lacks the Asp2
XX transmembrane domain and the Asp2 protein, and where the polypeptide and
XX the fragment retain the beta-secretase activity of the mammalian Asp2
XX protein. The invention also details polynucleotides for the Asp
XX proteins and vectors expressing them, and a polypeptide (isoform of
XX amyloid protein precursor (APP)) comprising the amino acid sequence of an
XX APP or its fragment containing an APP cleavage site recognizable by a
XX mammalian beta-secretase, and further comprising two lysine residues at
XX the carboxyl terminus of the amino acid sequence of the mammalian APP or
XX APP fragment. Also included in the invention are methods of identifying
XX modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
XX useful for treating Alzheimer's disease. APP is useful in methods for
XX identifying inhibitors or modulators of human Asp2 activity and
XX amyloid-beta (Abeta) peptide production. APP is also useful in designing
XX therapeutics for the treatment or prevention of Alzheimer's disease.
XX APP comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which
XX is associated with increased levels of Abeta processing is useful in
XX assays relating the Alzheimer's research. The expression vector is useful
XX for recombinantly expressing APP. Nucleic acids that hybridize to
XX Asp oligonucleotides are useful as probes or primers. The probes are
XX useful for detecting Hu-Asp nucleic acids in in vitro assays and in
XX Northern and Southern blots. The present sequence is an synthetic
XX peptide substrate for Asp2 corresponding to the APP swedish mutation
XX site, APP-SW.
XX Sequence 10 AA;
XX Query Match 100.0%; Score 44; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.0087;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SEVNLDADF 9
XX | | | | | | | |
XX Db 1 SEVNLDADF 9
XX Search completed: November 18, 2002, 12:52:14
XX Job time : 25.2609 secs

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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:41:03 ; Search time 37.7391 Seconds
(without alignments)
49.432 Million cell updates/sec

Title: US-09-724-571-97
Perfect score: 66
Sequence: 1 KTEISEVNLVAEF 14
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	14	21 AAB07888	A peptide fragment
2	65	98.5	19	22 AAE00612	PCBCI APP beta-sec
3	59	89.4	18	22 AAE00609	Beta-amyloid precu
4	59	89.4	19	22 AAE00611	Amyloid precursor
5	59	89.4	20	21 AAY69714	Beta-APP alpha-sec
6	59	89.4	20	21 AAU78509	Beta-amyloid precu
7	59	89.4	30	18 AAW08360	Beta-secretase sub
8	59	89.4	30	20 AAY33754	Synthetic oligopep
9	59	89.4	30	21 AAB07895	Substrate for beta
10	59	89.4	30	22 AAB47264	Peptide 26-4' SW, f

11	59	89.4	30	23 ABE09004	Peptide #2 used to
12	59	89.4	30	23 AAM50898	Oligopeptide subst
13	59	89.4	30	23 ABB07599	Synthetic oligopep
14	59	89.4	30	23 AAE16664	Oligopeptide subst
15	59	89.4	30	23 AAE16664	Synthetic amyloid
16	59	89.4	32	17 AAU04402	Mouse amyloid prec
17	59	89.4	32	17 AAW04403	Mouse amyloid prec
18	59	89.4	32	17 AAW04401	Mouse amyloid prec
19	59	89.4	32	23 ABB08999	Amyloid precursor
20	59	89.4	32	23 ABB07594	Biotinylated synth
21	59	89.4	32	23 AAE16659	APP substrate pept
22	59	89.4	32	23 AAE16659	Synthetic amyloid
23	59	89.4	33	18 AAW08359	Beta-secretase sub
24	59	89.4	33	20 AAY33753	Synthetic oligopep
25	59	89.4	33	21 AAB07892	Substrate for beta
26	59	89.4	33	22 AAB47263	Peptide 17-16' SW,
27	59	89.4	33	23 ABB09001	Peptide 17-16' SW,
28	59	89.4	33	23 AAM50893	Fluorescent substr
29	59	89.4	33	23 AAM50893	P26-P4' SW substr
30	59	89.4	33	23 ABB07596	Biotinylated synth
31	59	89.4	33	23 AAE16661	P26-P4' SW substr
32	59	89.4	33	23 AAE16661	Synthetic amyloid
33	59	89.4	39	21 AAY69718	Synthetic amyloid
34	59	89.4	42	18 AAW08350	Beta-APP alpha-sec
35	59	89.4	42	20 AAY33752	Wild type APP beta
36	59	89.4	42	22 AAB47262	Synthetic oligopep
37	59	89.4	58	20 AAW97997	Peptide 26-16' SW,
38	59	89.4	115	20 AAW98001	Swedish-FAD APP714
39	59	89.4	115	20 AAW98000	Swedish-FAD APP po
40	59	89.4	261	22 AAE00610	Chimeric cassette
41	59	89.4	506	19 AAW61152	Maltose binding pr
42	59	89.4	506	20 AAY33742	MBP-APP (SW192) fu
43	59	89.4	506	22 AAB47258	MBP-APP C-125 (Swe
44	59	89.4	695	21 AAY88435	Human APP695-sw va
45	59	89.4	695	22 AAE10633	Human amyloid prot

ALIGNMENTS

RESULT 1
AAB07888
ID AAB07888 standard; peptide; 14 AA.
XX AAB07888;
AC AAB07888;
XX 14-NOV-2000 (first entry)
DT A peptide fragment derived from beta-amyloid precursor protein.
DE Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.
XX Homo sapiens.
OS Homo sapiens.
XX WO200047618-A2.
PN WO200047618-A2.
XX 17-AUG-2000.
XX 10-FEB-2000; 2000WO-US03819.
XX 10-FEB-1999; 99US-0119571.
PR 15-JUN-1999; 99US-0139172.
XX (ELAN-) ELAN PHARM INC.
XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
XX WPI; 2000-533011/48.
DR Purified beta-secretase protein used in assays to discover inhibitors
PT

The present amino acid sequence is a pCIB1 plasmid amyloid precursor protein (APP) beta-secretase cleavage site (AAE00611) (D/I) mutant. APP

The present sequence is a beta-secretase cleavage site of beta-amyloid

CC precursor protein (beta-APP) mutant found in certain families of
 CC autosomal dominant form of Alzheimer's disease. This sequence is used to
 CC construct a chimeric cassette comprising human caspase-3 with interdomain
 CC linker replaced by this sequence. This modified caspase-3 plays a pivotal
 CC role in Alzheimer's disease. Caspases are a family of cysteine proteases,
 CC that participate in the initiation and execution of apoptosis.
 CC The present invention relates to a method for functional cloning of genes
 CC encoding proteins or enzymes involved in proteolytic cleavage. The
 CC invention is based on the use of caspase expression cassettes comprising
 CC the coding sequence of a proteolytic cleavage site flanked by sequences
 CC encoding two caspase subunits. A fusion polypeptide comprising a first
 CC and a second caspase subunit, separated by a cleavage site not associated
 CC in nature, is useful for cloning gene encoding enzymes involved in
 CC proteolytic cleavage. An expression cassette containing fusion
 CC polypeptide is used to identify a mutant cell line deficient in an
 CC enzyme of interest and is also useful for diagnosis and suppression of
 CC proliferation or metastases of a tumour cell characterised by
 CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
 CC selectively expressed in the tumour cells). DNA encoding fusion
 CC polypeptide is used in gene therapy.
 XX
 SQ Sequence 18 AA;

Query Match 89.4%; Score 59; DB 22; Length 18;
 Best Local Similarity 92.9%; Pred. No. 0.00079;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEETSEVNLVAEF 14
 |||||
 DB 1 KTEETSEVNLDAEF 14

RESULT 4
 AAE00611
 ID AAE00611 standard; peptide; 19 AA.
 XX
 AC AAE00611;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Amyloid precursor protein (APP) beta-secretase cleavage site.
 XX
 KW Amyloid precursor protein; APP; caspase; beta-secretase; cleavage site;
 KW cysteine protease; apoptosis; caspase expression cassette; metastasis;
 KW tumour; cathepsin B; urokinase; proliferation; gene therapy;
 KW interdomain linker; Alzheimer's disease.
 XX
 OS Unidentified.
 XX
 PN WO200129232-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 19-OCT-2000; 2000WO-US28941.
 XX
 PR 20-OCT-1999; 99US-0160559.
 PR 14-AUG-2000; 2000US-0225564.
 XX
 PA (SCIO-) SCTOS INC.
 XX
 PI Cordell B, Li Y;
 XX
 DR WPI; 2001-290920/30.
 XX
 XX Novel fusion polypeptide comprising first and second caspase subunit
 PT separated by cleavage site not associated in nature with caspase
 PT subunit, useful for cloning gene encoding enzymes involved in
 PT proteolytic cleavage -
 XX
 PS Disclosure; Fig 28A; 116pp; English.
 XX
 CC The present amino acid sequence is a beta-secretase cleavage site of
 CC an amyloid precursor protein (APP). This sequence is used to construct

CC an artificially engineered chimeric cassette comprising human caspase-3
 CC with interdomain linker replaced by swedish mutant beta-secretase
 CC cleavage site. This modified caspase-3 plays a pivotal role in
 CC Alzheimer's disease. Caspases are a family of cysteine proteases, that
 CC participate in the initiation and execution of apoptosis.
 CC The present invention relates to a method for functional cloning of genes
 CC encoding proteins or enzymes involved in proteolytic cleavage. The
 CC invention is based on the use of caspase expression cassettes comprising
 CC the coding sequence of a proteolytic cleavage site flanked by sequences
 CC encoding two caspase subunits. A fusion polypeptide comprising a first
 CC and a second caspase subunit, separated by a cleavage site not associated
 CC in nature, is useful for cloning gene encoding enzymes involved in
 CC proteolytic cleavage. An expression cassette containing fusion
 CC polypeptide is used to identify a mutant cell line deficient in an
 CC enzyme of interest and is also useful for diagnosis and suppression of
 CC proliferation or metastases of a tumour cell characterised by
 CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,
 CC selectively expressed in the tumour cells). DNA encoding fusion
 CC polypeptide is used in gene therapy.
 XX
 SQ Sequence 19 AA;

Query Match 89.4%; Score 59; DB 22; Length 19;
 Best Local Similarity 92.9%; Pred. No. 0.00084;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEETSEVNLVAEF 14
 |||||
 DB 2 KTEETSEVNLDAEF 15

RESULT 5
 AAY69714
 ID AAY69714 standard; peptide; 20 AA.
 XX
 AC AAY69714;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Beta-APP alpha-secretase substrate [NL]-APP(-10,+10).
 XX
 KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;
 KW cleavage site; beta-secretase; neurodegenerative disease;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9964587-A1.
 XX
 PD 16-DEC-1999.
 XX
 PF 04-JUN-1999; 99WO-FR01326.
 XX
 PR 05-JUN-1998; 98FR-0007068.
 PR 31-MAR-1999; 99US-0122599.
 XX
 PA (RHON) RHONE-POULENC RORER SA.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.
 XX
 PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;
 XX
 DR WPI; 2000-097537/08.
 XX
 XX Polypeptide with beta-secretase activity, specific for wild-type
 PT amyloid precursor protein, useful in treating Alzheimer's disease -
 XX
 PS Example 3; Page 24; 44pp; French.
 XX
 CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a
 CC novel polypeptide with beta-secretase activity that can cleave
 CC specifically the natural beta-amyloid precursor protein (bAPP). Normal
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and

CC Val636-Ile637 (positions 4-5 and 44-45 of AAV69701). The novel
 CC polypeptide is used to identify agents that interact specifically with
 CC it. These agents regulate metabolism of APP, particularly they slow down
 CC or reduce production of beta-amyloid, so can be used to treat
 CC neurodegenerative diseases, particularly Alzheimer's disease.

XX
 XX
 XX Sequence 20 AA;
 Query Match 89.4%; Score 59; DB 21; Length 20;
 Best Local Similarity 92.9%; Pred. No. 0.00089;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
 Db 1 KTEEISEVNLDAEF 14
 |||||

RESULT 6
 AAU78509
 ID AAU78509 standard; Peptide: 20 AA.
 AC AAU78509;
 XX

DT 18-JUN-2002 (first entry)
 DE Beta amyloid precursor protein beta secretase cleavage site.
 XX
 XX Alzheimer's disease; beta amyloid precursor protein; beta secretase;
 KW BACE; beta-site APP cleaving enzyme; neurotropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 KW BACE secretase/sheddase; neurodegenerative disorder.

XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 10..11
 FT /note= "Beta secretase cleavage site"

XX WO200210354-A2.
 XX
 XX 07-FEB-2002.
 XX
 XX 01-AUG-2001; 2001WO-CA01118.
 XX
 XX 01-AUG-2000; 2000CA-2313828.
 PR
 XX (RECL-) INST RECH CLINIQUES MONTREAL.

XX Seidah NG, Chretien M, Cromlish JA;
 PI WPI; 2002-280632/32.
 XX

XX Modulating activity of beta-site amyloid precursor protein-cleaving
 PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
 PT characterised by generation of Abeta protein, by preventing cleavage of
 PT enzyme -
 XX
 XX Disclosure; Page 21; 64pp; English.

XX This invention relates to a novel method for modulating activity of
 CC beta-site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable
 CC of hybridising with BACE mRNA, by using a ribozyme that targets and
 CC degrades BACE secretase mRNA, with a peptide that can interfere with
 CC binding of the enzyme with BACE or using an antibody or antagonist that
 CC can function as an inhibitor of BACE secretase activation. The methods
 CC of the invention modulate the activity of BACE secretase/sheddase by
 CC preventing cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta

CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised
 CC by the generation of Abeta protein by measuring the levels of BACE
 CC C terminal cleavage products in a sample or tissue where an increase
 CC in cleavage products indicates a person at risk. The present sequence
 CC represents the Beta secretase cleavage site of the beta amyloid
 CC precursor protein, this sequence was used to assay beta secretase
 CC activity of different BACE mutants of the invention.

XX
 XX Sequence 20 AA;
 Query Match 89.4%; Score 59; DB 23; Length 20;
 Best Local Similarity 92.9%; Pred. No. 0.00089;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
 Db 1 KTEEISEVNLDAEF 14
 |||||

RESULT 7
 AAU08360
 ID AAU08360 standard; peptide; 30 AA.

XX
 XX AC AAU08360;
 XX
 XX 05-SEP-1997 (first entry)
 XX
 XX Beta-secretase substrate #2.

XX Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
 KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
 XX Synthetic.

XX WO9640885-A2.
 XX
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US09985.
 XX
 XX 07-JUN-1995; 95US-0485152.
 PR 07-JUN-1995; 95US-0480498.
 XX
 XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Anderson JP, Chrysler SMS, Jacobson-croak KL, Kelm PS;
 PI Mcconlogue LC, Sinha S, Tan H;
 XX WPI; 1997-052304/05.

XX Beta-secretase which specifically cleaves beta-amyloid precursor
 PT protein - useful to screen for inhibitors useful in treatment of
 PT Alzheimer's disease
 XX

XX Disclosure; Page 45; 92pp; English.
 XX
 XX AAU08359-W08362 represent substrates for the enzyme of the invention.
 CC The enzyme of the invention is beta-secretase, and specifically cleaves
 CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP
 CC is thought to occur via cleavage between residues 16 and 17 of the
 CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing
 CC is thought to occur by beta-secretase cleavage of beta-APP.
 CC Beta-secretase activity can be detected and measured using a method of
 CC the invention, which detects at least one of the beta-secretase cleavage
 CC products formed on cleavage. The method can be used to determine whether
 CC a test substance inhibits proteolytic cleavage, by beta-secretase, of
 CC beta-APP. Compounds effective to at least partially inhibit
 CC beta-secretase activity can be used to inhibit cleavage of beta-APP in

CC cells or mammalian hosts. Isolation and purification of beta-secretase
CC will permit chemical modelling of a critical event in the pathology of
CC Alzheimer's disease.
XX
SQ Sequence 30 AA;

Query Match 89.4%; Score 59; DB 18; Length 30;
Best Local Similarity 92.9%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
|||||
Db 17 KTEEISEVNLDAEF 30

RESULT 8
AAV33754
ID AAY33754 standard; Protein; 30 AA.

XX
AC AAY33754;

XX 09-NOV-1999 (first entry)

XX Synthetic oligopeptide 26-4'SW.

XX Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome;
KW Alzheimer's disease; measure activity; cleavage site.
XX
OS Synthetic.

XX US5942400-A.

XX 24-AUG-1999.

XX 07-JUN-1996; 96US-0659984.

XX 07-JUN-1996; 96US-0659984.

XX 07-JUN-1995; 95US-0480498.

XX 07-JUN-1995; 95US-0485152.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Jacobson-Croak KL, Sinha S;

XX WPI; 1999-517417/43.

XX A method for detecting human beta-secretase cleavage of polypeptides
XX useful for identifying beta-secretase inhibitors

XX Examples; Column 30; 43pp; English.

XX Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring
CC the activity of beta-secretase (AAY33741). Beta-secretase is capable of
CC cleaving beta-amyloid protein precursor (APP) (AAY33742). These
CC synthetic peptides contain the cleavage site of APP. Beta-secretase and
CC APP are used in a method for detecting human beta-secretase cleavage of
CC polypeptides and for identifying beta-secretase inhibitors. Inhibition
CC of beta-secretase activity would be useful for chemical modelling of a
CC critical event in the pathology of Alzheimer's disease. Inhibitors of
CC beta-secretase would be useful for the prevention and treatment of
CC Alzheimer's disease and Down's Syndrome.

XX Sequence 30 AA;

Query Match 89.4%; Score 59; DB 20; Length 30;
Best Local Similarity 92.9%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
|||||
Db 17 KTEEISEVNLDAEF 30

RESULT 9
AAB07895

ID AAB07895 standard; Peptide; 30 AA.

XX
AC AAB07895;

XX 14-NOV-2000 (first entry)

XX Substrate for beta-secretase enzyme.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KW inhibitor.

XX Synthetic.

XX Key Location/Qualifiers
FT Cleavage-site 26..27

XX WO200047618-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US03819.

XX 10-FEB-1999; 99US-0119571.

XX 15-JUN-1999; 99US-0139172.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

XX Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
XX which can be used for the treatment of amyloidogenic diseases e.g.
XX Alzheimer's disease -

XX Example 4; Page 71; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to
CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence represents a peptide substrate used to test the
CC activity of beta-secretase enzyme.

XX Sequence 30 AA;

Query Match 89.4%; Score 59; DB 21; Length 30;
Best Local Similarity 92.9%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTEEISEVNLVAEF 14
|||||
Db 17 KTEEISEVNLDAEF 30

RESULT 10

AAB47264
ID AAB47264 standard; Peptide; 30 AA.

XX
AC AAB47264;

XX 18-JUL-2001 (first entry)

XX Peptide 26-4'SW, for used in beta-secretase assay.

XX Beta-secretase; isotype; beta-amyloid precursor protein; APP;
 KW beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syndrome;
 KW HCHWA-D; Swedish mutation; maltose binding protein; MBP.
 OS Synthetic.
 XX US6221645-B1.
 XX 24-APR-2001.
 XX 07-JUN-1996; 960S-0660531.
 XX 07-JUN-1995; 950S-0480498.
 XX (ELAN-) ELAN PHARM INC.
 XX Chrysler SMS, Sinha S, Keim PS, Anderson JP, Tan H, McConlogue LC;
 XX WPI; 2001-315578/33.
 XX Novel antibody that specifically binds native beta-secretase protein,
 PT useful for raising anti-idiotypic antibodies and for detecting or
 PT diagnosing pathological conditions related to presence of respective
 PT antigens.
 XX Example; Column 29; 42pp; English.
 XX The sequences given in AAB47262-67 represent synthetic peptides
 CC containing the cleavage sites derived from wild-type beta-amyloid
 CC precursor protein (APP). These peptides were used in assays utilising
 CC partially purified beta-secretase to identify beta-secretase inhibitors.
 CC Beta-secretase is thought to be responsible for the pathogenic
 CC processing of APP to form beta amyloid peptide (beta-AP) in beta-AP
 CC related conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D
 CC etc. Beta-secretase has a molecular weight of 260-300 kD and will bind
 CC to wheat germ agglutinin but not to concanavalin A. Beta-secretase
 CC will cleave both the wild type and the Swedish mutation of APP.
 XX Sequence 30 AA;
 SQ
 Query Match 89.4%; Score 59; DB 22; Length 30;
 Best Local Similarity 92.9%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KTEEISEVNLVAEF 14
 Db 17 KTEEISEVNLDAEF 30
 |||||
 RESULT 11
 ID ABB09004
 XX ABB09004 standard; peptide; 30 AA.
 AC ABB09004;
 XX 19-JUN-2002 (first entry)
 DT Peptide #2 used to assay secretase activity.
 XX
 DE Amyloid precursor protein; APP; Alzheimer's disease; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; antiparkinsonian;
 KW Down's syndrome; cerebral amyloid angiopathy; dementia.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Cleavage-site 26..27
 FT /note= "Beta secretase cleavage site"
 XX WC200202505-A2.
 PN 10-JAN-2002.
 XX

XX 29-JUN-2001; 2001WO-US20852.
 XX 30-JUN-2000; 2000US-215323P.
 XX (ELAN-) ELAN PHARM INC.
 XX Fang LY, Hom R, John V, Maillaird M;
 XX WPI; 2002-171625/22.
 XX New substituted amines are e.g. beta-amyloid peptide inhibitors, useful
 PT for treating Alzheimer's disease, mild cognitive impairment and Down's
 PT syndrome.
 XX Example D; Page 97; 136pp; English.
 XX This invention relates to substituted amines and their salts, which
 CC are neurotropic, neuroprotective, cerebroprotective, haemostatic and
 CC antiparkinsonian in their action. They are used in the preparation of
 CC a composition useful for treating, preventing or delaying the on-set
 CC of Alzheimer's disease, for treating mild cognitive impairment, Down's
 CC syndrome, cerebral amyloid angiopathy, dementia associated with
 CC Parkinson's disease, dementia associated with progressive supranuclear
 CC palsy, and dementia associated with cortical basal degeneration.
 CC They are also useful for treating diseases characterised by beta-amyloid
 CC deposits in brain, and for producing beta-secretase complexes. This
 CC sequence represents a peptide that incorporate the known cleavage
 CC site of beta-secretase. This substrate is used to assay
 CC beta-secretase activity.
 XX Sequence 30 AA;
 SQ
 Query Match 89.4%; Score 59; DB 23; Length 30;
 Best Local Similarity 92.9%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KTEEISEVNLVAEF 14
 Db 17 KTEEISEVNLDAEF 30
 |||||
 RESULT 12
 AAM50898
 ID AAM50898 standard; Peptide; 30 AA.
 XX AAM50898;
 XX 07-MAY-2002 (first entry)
 DT Oligopeptide substrate for beta-secretase.
 XX Beta-secretase; substrate; amyloid precursor protein;
 KW APP; amyloid beta peptide; inhibitor; screening;
 KW neurodegenerative disorder; cognitive impairment; Down's syndrome;
 KW Alzheimer's disease; hereditary cerebral haemorrhage;
 KW cerebral amyloid angiopathy; dementia; therapy.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Cleavage-site 26..27
 FT WC200202512-A2.
 XX 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US21012.
 XX 30-JUN-2000; 2000US-215323P.
 XX 22-NOV-2000; 2000US-252736P.
 XX 15-DEC-2000; 2000US-255956P.
 XX 13-FEB-2001; 2001US-268497P.
 XX

PR 29-MAR-2001; 2001US-279779P.
 XX 04-JUN-2001; 2001US-295589P.
 PA (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX Maillaird M, Hom C, Gallunas A, Jagodzinska B, Fang LY, John V;
 PI Freskos JN, Pulley SR, Beck JP, Tenbrink RE;
 XX WPI; 2002-171627/22.
 DR New substituted amines are e.g. amyloid beta peptide production
 XX inhibitors, useful for treating or preventing e.g. Alzheimer's disease,
 PT mild cognitive impairment and other degenerative diseases -
 XX Example D; Page 344; 651pp; English.
 XX The present sequence is that of a peptide that incorporates the
 CC known cleavage site of beta-secretase on amyloid precursor protein
 CC (APP). The peptide, which may optionally be tagged with a
 CC fluorescent or chromogenic moiety, can be used in assays to
 CC determine the beta-secretase inhibitory activity of novel
 CC substituted amine compounds of the invention. Comparison of
 CC substrate cleavage results in the presence of an inhibitor and
 CC in the presence of a control provides a measure of the compound's
 CC inhibitory activity. Novel compounds of the invention are
 CC effective inhibitors of beta-secretase, inhibit beta-secretase
 CC mediated cleavage of APP, are effective inhibitors of A beta
 CC production, and/or effectively reduce amyloid beta deposits or
 CC plaques. They are used in the treatment or prevention of diseases
 CC characterised by amyloid deposits in the brain, e.g. for treating
 CC or preventing Alzheimer's disease (AD), for helping prevent or
 CC delay the onset of AD, for treating mild cognitive impairment or
 CC (MCI), preventing or delaying the onset of AD in those who would
 CC progress from MCI to AD, for treating Down's syndrome and
 CC hereditary cerebral haemorrhage with Amyloidosis of the Dutch
 CC type, for treating cerebral amyloid angiopathy and preventing its
 CC potential consequences i.e. single and recurrent lobar haemorrhages,
 CC for treating other degenerative dementias, including dementias
 CC of mixed vascular and degenerative dementias, dementia associated with
 CC Parkinson's disease, dementia associated with progressive
 CC supranuclear palsy, and dementia associated with cortical basal
 CC degeneration, and for treating diffuse Lewy body type of AD (all
 XX claimed).
 SQ Sequence 30 AA;
 Query Match 89.4%; Score 59; DB 23; Length 30;
 Best Local Similarity 92.9%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KTEISEVNLVAEF 14
 Db 17 KTEISEVNLDAEF 30
 RESULT 13
 ID ABB07599
 AC ABB07599 standard; peptide; 30 AA.
 AC ABB07599;
 XX 08-MAY-2002 (first entry)
 DT Synthetic oligopeptide substrate having beta-secretase cleavage site.
 DE APP; amine derivative; beta-secretase; amyloid precursor protein; A beta;
 XX amyloid beta peptide; beta-amyloid; neurotrophic; neuroprotective;
 KW cerebroprotective; haemostatic; antiparkinsonian.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX Key

FT Cleavage-site 26..27 /note= "beta-secretase cleavage site"
 XX WO200202520-A2.
 PN 10-JAN-2002.
 PD 02-JUL-2001; 2001WO-US21000.
 XX 30-JUN-2000; 2000US-215323P.
 PR 29-JUN-2001; 2001US-0895843.
 XX (ELAN-) ELAN PHARM INC.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX Beck JP, Gallunas A, Hom R, Jagodzinska B, John V, Maillaird M;
 PI WPI; 2002-188416/24.
 XX New substituted amine derivatives, useful for treating Alzheimer's
 PT disease and other degenerative diseases -
 XX Example D; Page 163; 286pp; English.
 XX The invention relates to substituted amine derivatives of specified
 CC formulae or their salts. The amine derivatives can inhibit beta-secretase
 CC activity or inhibit the cleavage of amyloid precursor protein (APP) in a
 CC reaction mixture. They can also be used to inhibit production of amyloid
 CC beta peptide (A beta) in a cell or inhibit production of beta-amyloid
 CC plaque in an animal. The amine derivatives are useful for treating or
 CC preventing a disease characterized by beta-amyloid deposits in the brain
 CC e.g. for treating or preventing Alzheimer's disease (AD), for helping
 CC prevent or delay the onset of AD, for treating mild cognitive impairment
 CC (MCI), preventing or delaying the onset of AD in those who would progress
 CC from MCI to AD, for treating Down's syndrome, humans who have hereditary
 CC cerebral haemorrhage with the Amyloidosis of the Dutch type, cerebral
 CC amyloid angiopathy and preventing its potential consequences i.e. single
 CC and recurrent lobar haemorrhages for treating other degenerative
 CC dementias, including dementias of mixed vascular and degenerative origin,
 CC dementia associated with Parkinson's disease, dementia associated with
 CC progressive supranuclear palsy, dementia associated with cortical basal
 CC degeneration, diffuse Lewy body type of Alzheimer's disease. Sequences
 CC ABB07598-599 are synthetic APP oligopeptide substrates containing the
 CC cleavage site of beta-secretase, used to assay beta-secretase activity.
 XX Sequence 30 AA;
 SQ Query Match 89.4%; Score 59; DB 23; Length 30;
 Best Local Similarity 92.9%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KTEISEVNLVAEF 14
 Db 17 KTEISEVNLDAEF 30
 RESULT 14
 ID AAE16664
 AC AAE16664 standard; peptide; 30 AA.
 AC AAE16664;
 XX 09-APR-2002 (first entry)
 DT Oligopeptide substrate #2, used in the assay of the invention.
 DE Disubstituted amine derivative; Alzheimer's disease; Down's syndrome;
 XX degenerative disease; beta-amyloid deposit; mild cognitive impairment;
 KW hereditary cerebral haemorrhage; amyloidosis; degenerative dementia;
 KW cerebral amyloid angiopathy; Parkinson's disease; supranuclear palsy;
 XX cortical basal degeneration; AD; MCI; amyloid precursor protein;
 KW beta-secretase; amyloid beta peptide; A beta peptide.

OS Unidentified.

XX Key Location/Qualifiers

FH Cleavage-site 26...27

FT FT

XX WO200202518-A2.

PN 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US20856.

XX 30-JUN-2000; 2000US-215323P.

XX (ELAN-) ELAN PHARM INC.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Beck JP, Gailunas A, Hom R, Jagodzinska B, John V, Maillaird M;

XX WPI; 2002-122550/16.

XX New substituted amine derivatives, useful for treating Alzheimer's

XX disease and other degenerative diseases -

XX Example D; Page 163; 286pp; English.

XX The invention relates to substituted amine derivative compounds

XX useful for treating Alzheimer's disease and other degenerative diseases.

XX Compounds of the invention possess beta secretase inhibitory activity and

XX are useful for inhibiting beta-secretase mediated cleavage of amyloid

XX precursor protein (APP) and particularly, to inhibit the production of

XX amyloid beta (A beta) peptide. They are useful for treating or preventing

XX a disease characterised by beta-amyloid deposits in the brain e.g. for

XX treating or preventing Alzheimer's disease (AD), for helping to prevent

XX or delay the onset of Alzheimer's disease, for treating mild cognitive

XX impairment (MCI), Down's syndrome, hereditary cerebral haemorrhage with

XX the amyloidosis of the Dutch type, cerebral amyloid angiopathy and

XX preventing its potential consequences i.e. single and recurrent lobar

XX haemorrhages, for treating other degenerative dementias including

XX dementias of mixed vascular and degenerative origin, dementia associated

XX with Parkinson's disease, dementia associated with progressive

XX supranuclear palsy, dementia associated with cortical basal degeneration

XX and diffuse Lewy body type of Alzheimer's disease. The present sequence

XX is oligopeptide substrate used in assay of the invention.

XX

SQ Sequence 30 AA;

Query Match 89.4%; Score 59; DB 23; Length 30;

Best Local Similarity 92.9%; Pred. No. 0.0014; 1; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0;

QY 1 KTEEISEVNLVAEF 14

Db 17 KTEEISEVNLDAEF 30

RESULT 15

AAU74838

ID AAU74838 standard; Peptide: 30 AA.

XX AAU74838;

XX 09-APR-2002 (first entry)

XX Synthetic amyloid precursor protein (APP) oligopeptide substrate #2.

XX Amyloid precursor protein; APP; Alzheimer's disease; amine XV;

XX nontropic; neuroprotective; cerebroprotective; haemostatic;

XX antiparkinsonian; beta-secretase; amyloid beta peptide; amyloidosis;

XX beta-amyloid plaque; mild cognitive impairment; MCI; Down's syndrome;

XX hereditary cerebral haemorrhage; cortical basal degeneration;

XX cerebral amyloid angiopathy; lobar haemorrhage; degenerative dementia;

XX Parkinson's disease; supranuclear palsy; dementia.

OS Synthetic.

XX Key Location/Qualifiers

FH Cleavage site 26...27

FT /note- "Beta-secretase cleavage site"

XX WO200202506-A2.

PN 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US20930.

XX 30-JUN-2000; 2000US-215323P.

XX (ELAN-) ELAN PHARM INC.

XX Fang LY, John V;

XX WPI; 2002-147995/19.

XX New substituted amines are e.g. amyloid beta peptide production

XX inhibitors, useful for treating or preventing e.g. Alzheimer's disease,

XX mild cognitive impairment and other degenerative diseases -

XX Example D; Page 118; 434pp; English.

XX This invention relates to a novel substituted amine of formula XV and

XX its salts which can be used to treat Alzheimer's disease and similar

XX diseases. The compound of the invention may have nootropic,

XX neuroprotective, cerebroprotective, haemostatic and antiparkinsonian

XX activities. The amine acts as a beta-secretase activity inhibitor,

XX inhibiting cleavage of amyloid precursor protein (APP) and the

XX formation of amyloid beta peptide and beta-amyloid plaque production.

XX The amine of the invention is useful for treating or preventing a

XX disease characterised by beta-amyloid deposits in the brain e.g.

XX Alzheimer's disease (AD), for treating mild cognitive impairment (MCI),

XX preventing or delaying the onset of Alzheimer's disease in those who

XX would progress from MCI to AD, for treating Down's syndrome, humans who

XX have hereditary cerebral haemorrhage with the Amyloidosis of the Dutch

XX type, cerebral amyloid angiopathy and preventing its potential

XX consequences i.e. single and recurrent lobar haemorrhages, for treating

XX other degenerative dementias, including dementias of mixed vascular and

XX degenerative origin, dementia associated with Parkinson's disease,

XX dementia associated with progressive supranuclear palsy, dementia

XX associated with cortical basal degeneration and diffuse Lewy body type

XX of Alzheimer's disease. The present sequence represents a synthetic

XX APP oligopeptide substrate #2 for the beta secretase enzyme. This

XX synthetic substrate was used to test the efficiency of the amine as an

XX inhibitor of beta secretase enzyme activity.

XX

SQ Sequence 30 AA;

Query Match 89.4%; Score 59; DB 23; Length 30;

Best Local Similarity 92.9%; Pred. No. 0.0014; 1; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 1;

QY 1 KTEEISEVNLVAEF 14

Db 17 KTEEISEVNLDAEF 30

Search completed: November 18, 2002, 12:52:14

Job Time : 37.7391 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 12:41:03 ; Search time 24.2609 Seconds
(without alignments)
49.432 Million cell updates/sec

Title: US-09-724-571-83
Perfect score: 44
Sequence: 1 SEVNLDAEF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_101002.:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	19	AAW82081
2	44	100.0	9	21	AAW87874
3	44	100.0	9	21	AAW87894
4	44	100.0	9	22	AAG73297
5	44	100.0	9	23	ABW09003
6	44	100.0	9	23	ABW050897
7	44	100.0	9	23	ABW07598
8	44	100.0	9	23	AAW16663
9	44	100.0	9	23	AAW74837
10	44	100.0	10	18	AAW08362

11	44	100.0	10	20	AAW33756
12	44	100.0	10	21	AAW69707
13	44	100.0	10	22	AAE10653
14	44	100.0	10	22	AAE06898
15	44	100.0	10	22	AAU06627
16	44	100.0	10	22	AAU07226
17	44	100.0	10	22	AAE02605
18	44	100.0	10	22	AAW47266
19	44	100.0	10	22	AAW66575
20	44	100.0	10	22	AAW61337
21	44	100.0	10	23	AAU59491
22	44	100.0	10	23	ABW78614
23	44	100.0	10	23	ABW06423
24	44	100.0	11	22	AAW75142
25	44	100.0	11	22	AAW75145
26	44	100.0	11	22	AAW7469
27	44	100.0	12	23	ABW08996
28	44	100.0	12	23	ABW07591
29	44	100.0	12	23	AAE16656
30	44	100.0	12	23	AAU74830
31	44	100.0	13	23	ABW06591
32	44	100.0	13	23	AAW50890
33	44	100.0	16	21	AAW06316
34	44	100.0	18	22	AAE00609
35	44	100.0	19	22	AAE00611
36	44	100.0	20	19	AAW82211
37	44	100.0	20	21	AAW69714
38	44	100.0	20	22	AAG73229
39	44	100.0	20	23	AAW78509
40	44	100.0	21	18	AAW08361
41	44	100.0	21	19	AAW82186
42	44	100.0	21	20	AAW33755
43	44	100.0	21	22	AAG73203
44	44	100.0	21	22	AAG73204
45	44	100.0	21	22	AAW47265

ALIGNMENTS

RESULT 1

AAW82081
ID AAW82081 standard; peptide; 9 AA.

XX
AC AAW82081;

DT 18-FEB-1999 (first entry)
XX

XX Fluorogenic protease indicator protease binding peptide #59.
DE

XX Protease activity; fluorophore; detection; fluorogenic; cellular uptake;
KW conformation change.
XX

XX Synthetic.
XX OS

XX WO9837226-A1.
PN

XX 27-AUG-1998.
PD

XX 20-FEB-1998; 98WO-US03000.
PF

XX 20-FEB-1997; 97US-0802981.
PR

XX (ONCO-) ONCOIMMUNIN INC.
PA

XX Komoriya A, Packard BS;
PI

XX WPI; 1998-467579/40.
DR

XX New fluorogenic compositions - containing 2 fluorophores separated
PT by a peptide comprising a protease binding site, used for detecting

PT protease activity in samples.
PT

Synthetic oligopep
Beta-APP alpha-sec
Human APP-Sw beta-
Human amyloid prec
Synthetic Asp2 rec
Human beta-amyloid
Human APP-Sw beta-
Peptide 5-5'SW, fo
Synthetic peptide
Swedish mutation p
Peptide #2 used as
Beta-secretase spe
Human APP Swedish
APP Swedish varian
Asp 1 substrate se
Asp2 substrate swe
Amyloid precursor
Biotinylated synth
APP substrate pept
Synthetic amyloid
Beta-secretase rel
Fluorescent substr
Human beta-amyloid
Beta-amyloid precu
Amyloid precursor
Fluorogenic protea
Beta-APP alpha-sec
Protease binding s
Beta amyloid precu
Beta-secretase sub
Fluorogenic protea
Synthetic oligopep
Protease binding s
Protease binding s
Peptide 5-16'SW, f

PS Claim 4; Page 77; 90pp; English.

XX AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformational changes in nucleic acids, oligosaccharides, polysaccharides, proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to a molecule can be used to enhance uptake by cells. The composition is composed of P - peptide comprising a protease binding site for the protease, F1, F2 peptides - fluorophores where F1 is attached to the amino terminal amino acid and S1, S2 peptides - when present, are attached to the carboxyl terminal amino acid and S1, S2 peptides - when present, are attached to the amino terminal amino acid, and S2, when present, is attached to the carboxyl terminal amino acid.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 2

AAAB07874
ID AAB07874 standard; peptide; 9 AA.

XX AC AAB07874;

XX DT 14-NOV-2000 (first entry)

XX DE A peptide fragment derived from beta-amyloid precursor protein.

XX KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.

XX KW Homo sapiens.

XX OS WO200047618-A2.

XX PN 17-AUG-2000.

XX PD 10-FEB-2000; 2000WO-US03819.

XX PF 10-FEB-1999; 99US-0119571.

XX PR 15-JUN-1999; 99US-0139172.

XX (ELAN-) ELAN PHARM INC.

XX PA Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M; Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L; WPI; 2000-533011/48.

XX PT Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.

XX PS Disclosure; Page 12; 121pp; English.

XX CC The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide substrate used to test the activity of beta-secretase enzyme.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

CC ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide derived from beta-amyloid precursor protein

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEVNLDAEF 9
Db 1 SEVNLDAEF 9

RESULT 3

AAAB07894
ID AAB07894 standard; Peptide; 9 AA.

XX AC AAB07894;

XX DT 14-NOV-2000 (first entry)

XX DE Substrate for beta-secretase enzyme.

XX KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.

XX KW Synthetic.

XX OS

XX FT Key

XX FT Cleavage-site 5..6

XX PN WO200047618-A2.

XX PD 17-AUG-2000.

XX PF 10-FEB-2000; 2000WO-US03819.

XX PR 10-FEB-1999; 99US-0119571.

XX PR 15-JUN-1999; 99US-0139172.

XX PA (ELAN-) ELAN PHARM INC.

XX PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M; Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L; WPI; 2000-533011/48.

XX PT Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.

XX PS Example 4; Page 71; 121pp; English.

XX CC The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide substrate used to test the activity of beta-secretase enzyme.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;

